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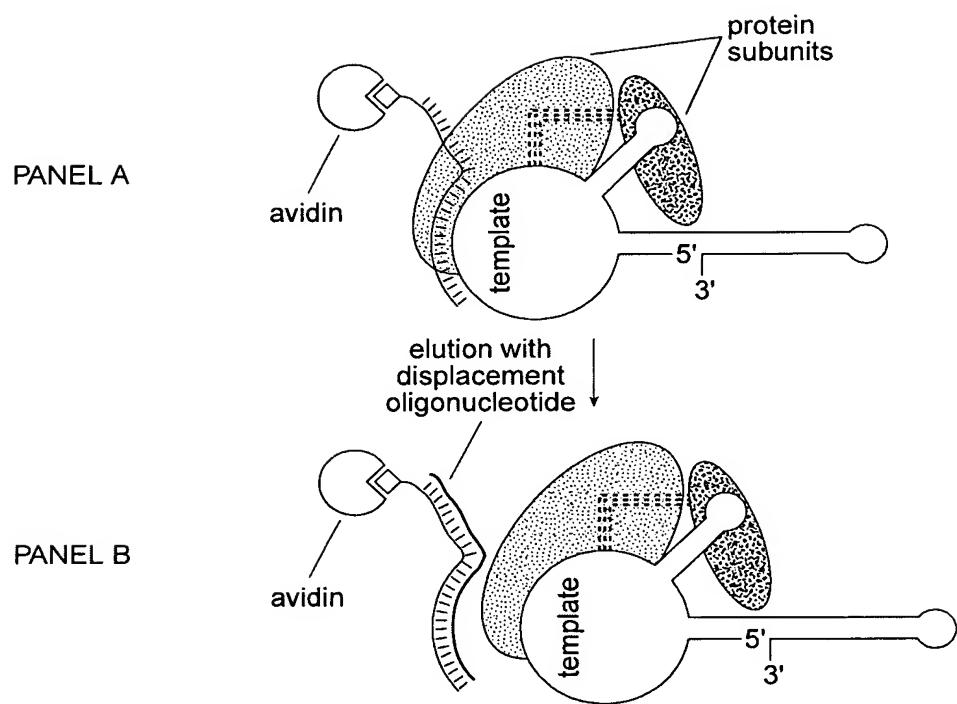
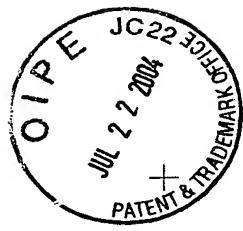
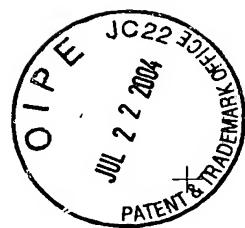


FIG. 1



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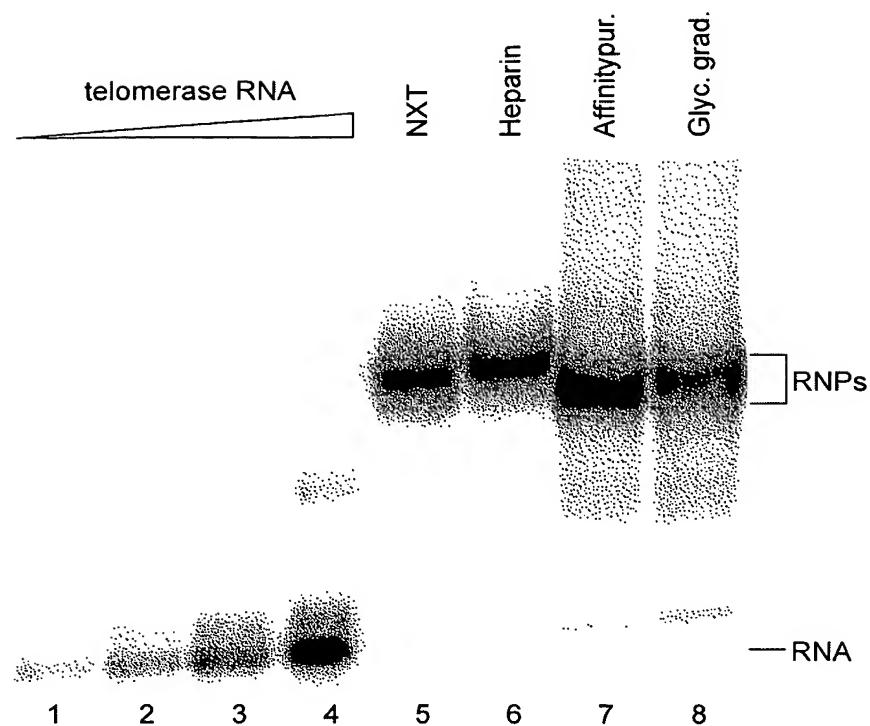


FIG. 2

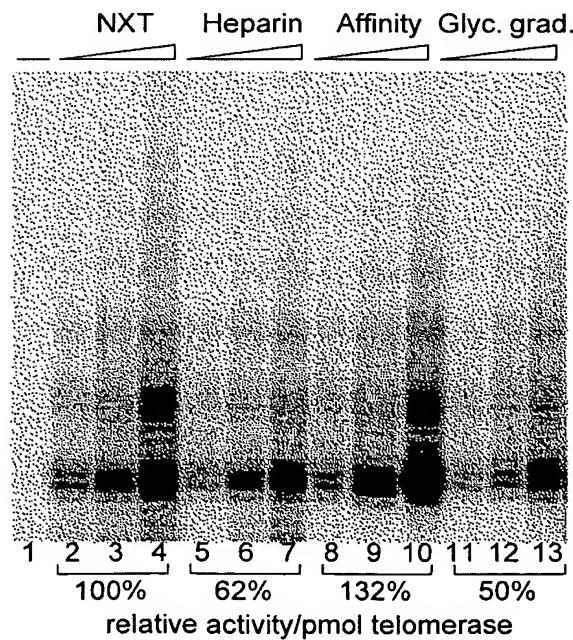
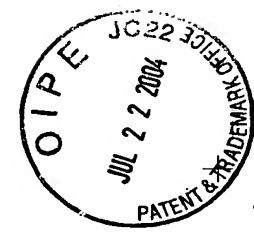


FIG. 3

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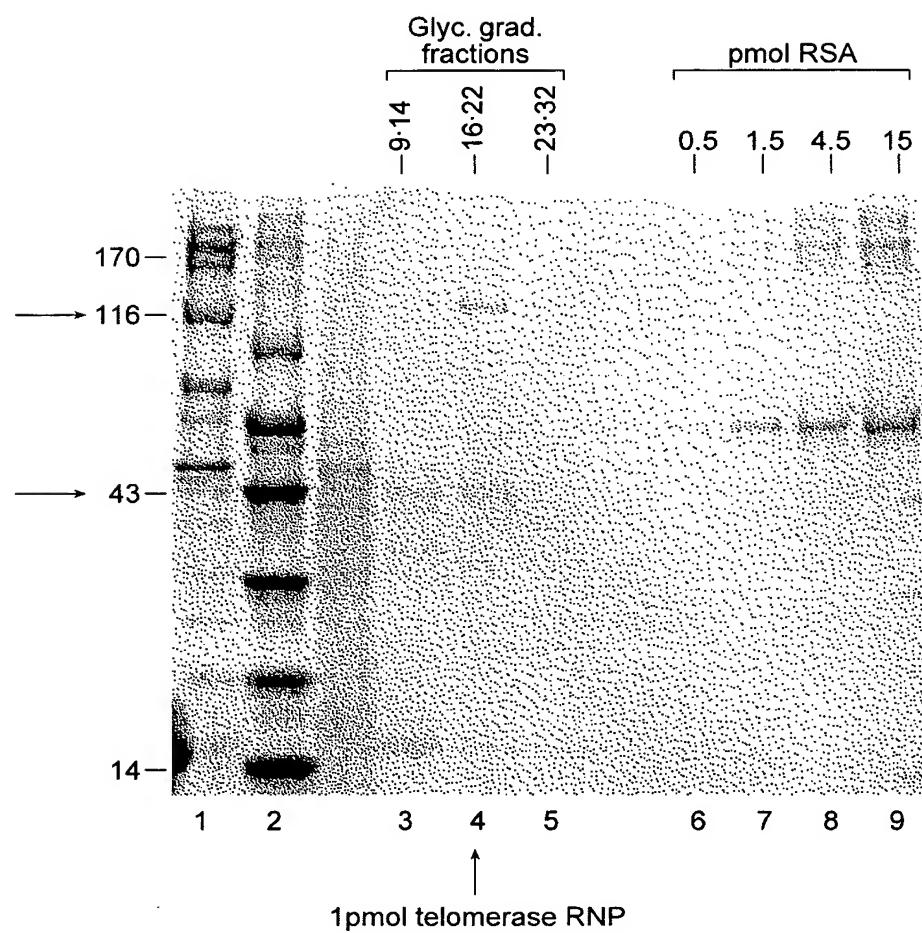
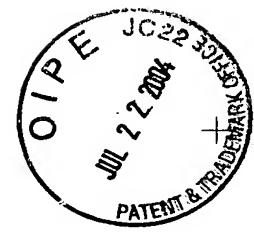


FIG. 4

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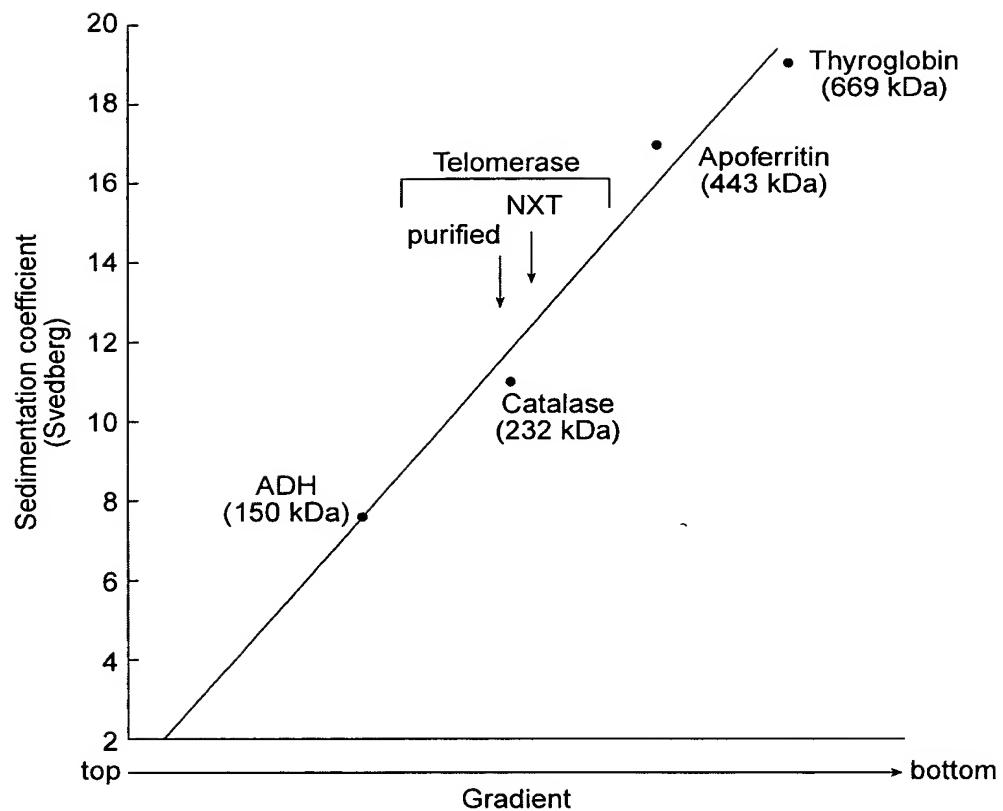
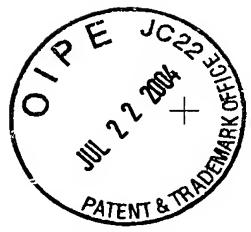


FIG. 5

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Telomerase:

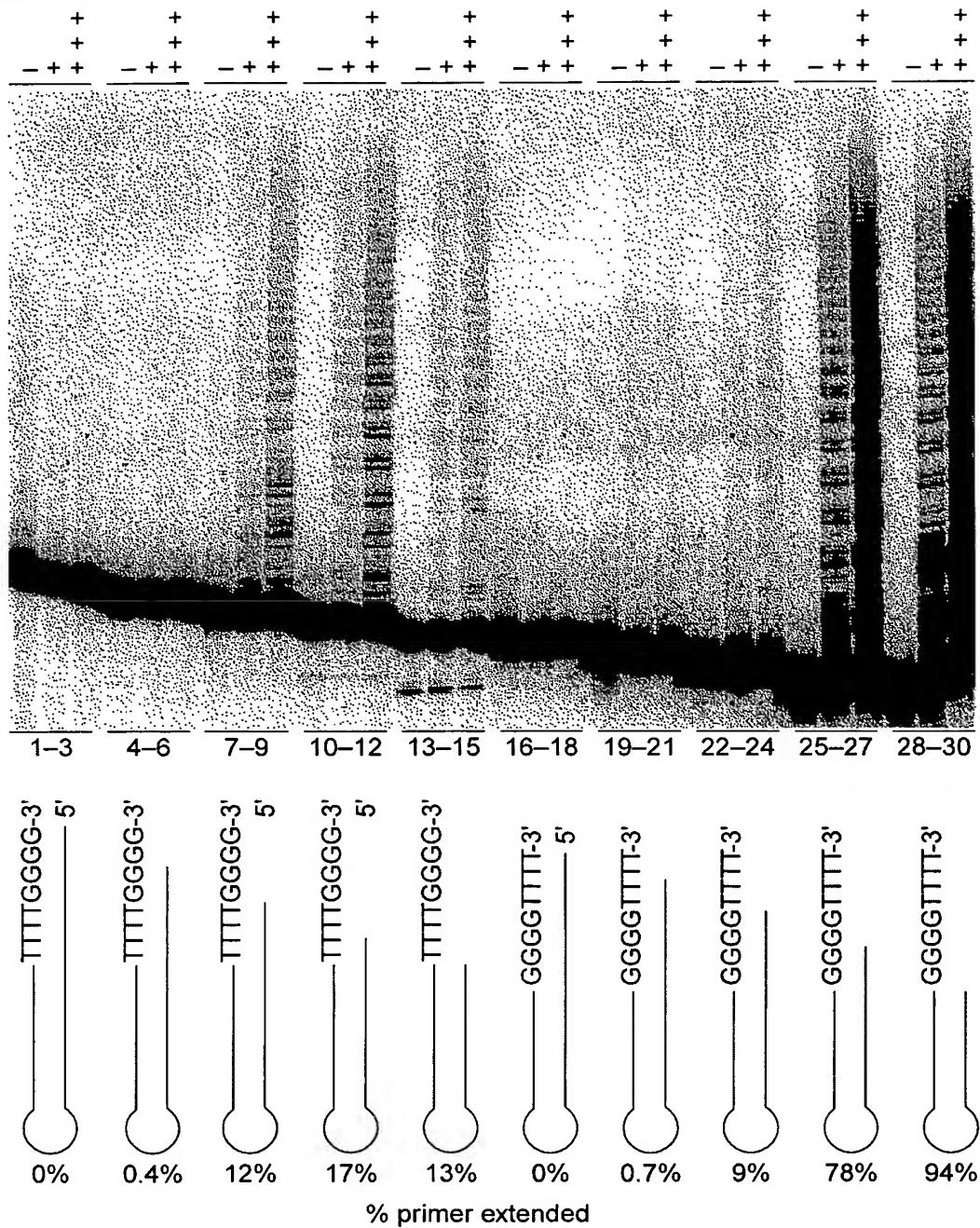
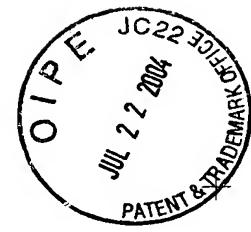


FIG. 6

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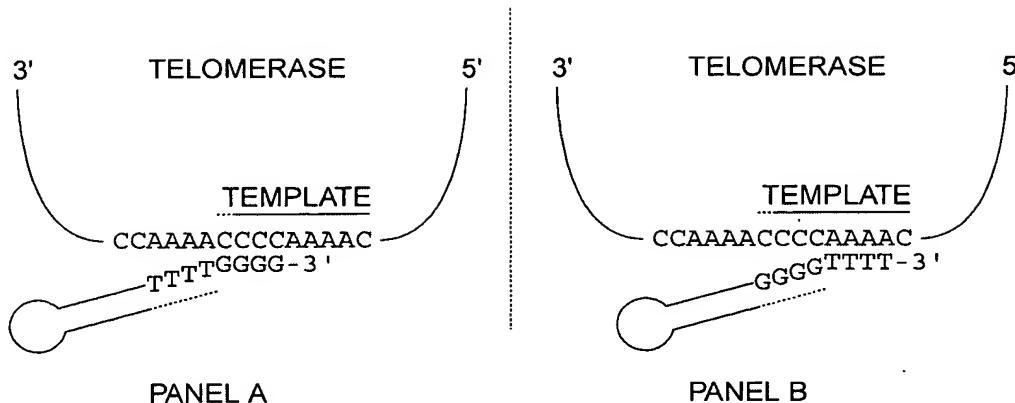
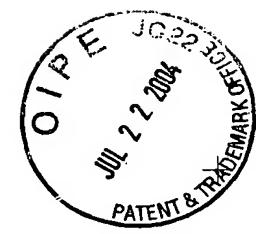


FIG. 7

1	CCCCAAAACC	CCAAAACCCC	AAAACCCCTA	TAAAAAAAGA	AAAAAATTGAG
51	GTAGTTAGA	AATAAAATAT	TATTCCCGCA	CAAATGGAGA	TGGATATTGA
101	TTGGATGAT	ATAGAAAATT	TACTTCCTAA	TACATTCAAC	AACTATAGCA
151	GCTCTTGTAG	TGACAAGAAA	GGATGCAAAA	CATTGAAATC	TGGCTCGAAA
201	TCGGCTTCAT	TGACTATTCC	AAAGTTGCAA	AAACAAATTAG	AGTTCTACTT
251	CTCGGATGCA	AATCTTATA	ACGATTCTTT	CTTGAGAAAA	TTAGTTTAA
301	AAAGCGGAGA	GCAAAGAGTA	GAAATTGAAA	CATTACTAAT	GTAAATAATAA
351	AATCAGGTAA	TGAGGATTAT	TCTATTTTTT	AGATCACTTC	TTAAGGAGCA
401	TTATGGAGAG	AATTACTTAA	TACTAAAGG	TAAACAGTT	GGATTATTTC
451	CCTAGCCAAC	AATGATGAGT	ATATAAATT	CATATGAGAA	TGAGTCAAAG
501	GATCTCGATA	CATCAGACTT	ACCAAAGACA	AACTCGCTAT	AAAACGCAAG
551	AAAAAGTTTG	ATAATCGAAC	AGCAGAAGAA	CTTATTGCAT	TTACTATTGCG
601	TATGGGTTTT	ATTACAATTG	TTTAGGTAT	CGACGGTGAA	CTCCCGAGTC
651	TTGAGACAAT	TGAAAAAGCT	GTTTACAAC	GAAGGAATCG	CAGTTCTGAA
701	AGTATCTGATG	TGTATGCCAT	TATTTGTGA	ATTAATCTCA	AATATCTTAT
751	CTCAATTAA	TGGATAGCTA	TAGAAACAAA	CCAAATAAAC	CATGCAAGTT
801	TAATGGAATA	TACGTTAAAT	CCTTTGGGAC	AAATGCACAC	TGAATTTATA
851	TTGGATTCTT	AAAGCATAGA	TACACAGAAT	GCTTTAGAGA	CTGATTTAGC
901	TTACAACAGA	TTACCTGTTT	TGATTACTCT	TGCTCATCTC	TTATATCTTT
951	AAAAGAAGCA	GGCGAAATGA	AAAGAAGACT	AAAGAAAGAG	ATTTCAAAAT
1001	TTGTTGATTC	TTCTGTAACC	GGATTAAACA	ACAAGAATAT	TAGCAACGAA
1051	AAAGAAGAG	AGCTATCACA	ATCCTGATTC	TTAAAGATTT	AAAAAATTCC
1101	AGGTAAAGAGA	GATACATTCA	TTAAAATTCA	TATATTATAG	TTTTTCATTT
1151	CACAGCTGTT	ATTTTCTTTT	ATCTAACAA	TATTTTTGGA	TTAGCTGGAA
1201	GTAAAAAGTA	TCAAATAAGA	GAAGCGCTAG	ACTGAGGTAA	CTTAGCTTAT
1251	TCACATTCA	AGATCGACCT	TCATATATCC	AATACGATGA	TAAGGAAACA
1301	GCAGTCATCC	GTTTTAAAAA	TAGTGCTATG	AGGACTAAAT	TTTTAGAGTC
1351	AAGAAATGGA	GCGAAATCT	TAATCAAAA	GAATTGCGTC	GATATTGCAA
1401	AAGAATCGAA	CTCTAAATCT	TTCTGTTATA	AGTAATTACCA	ATCTTGATTC
1451	ATTGAAGAGA	TTGACGAGGC	AACTGCACAG	AAGATCATT	AAGAAATAAA
1501	GTAACTTTA	TTAATTAGAG	AATAAACTAA	ATTACTAATA	TAGAGATCAG
1551	CGATCTTCAA	TTGACGAAAT	AAAAGCTGAA	CTAAAGTTAG	ACAATAAAA
1601	ATACAAACCT	TGGTCAAAAT	ATTGAGGAAG	GAAGAGAAGA	CCAGTTAGCA
1651	AAAGAAAAAA	TAAGGCAATA	AATAAAATGA	GTACAGAAGT	GAAGAAATAA
1701	AAGATTTATT	TTTTTCAATA	ATTATTGAA	AAGAGGGTT	TTGGGGTTTT
1751	GGGGTTTTGG	GG			

FIG. 11

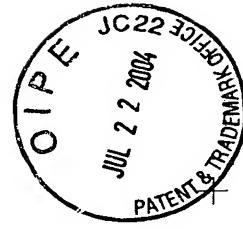


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FIG. 8

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1	AAAACCCCAA	AACCCCAAAA	CCCCTTTAG	AGCCCTGCAG	TTGGAAATAT
51	AACCTCAGTA	TTAATAAGCT	CAGATTTTAA	ATATTAATTAA	CAAAACCTAA
101	ATGGAGGTTG	ATGTTGATAA	TCAAGCTGAT	AATCATGGCA	TTCACTCAGC
151	TCTTAAGACT	TGTGAAGAAA	TTAAAGAAGC	AAAACGTTG	TACTCTTGGAA
201	TCCAGAAAGT	TATTAGATGA	AGAAATCAAT	CTCAAAGTCA	TTATAAAGAT
251	TTAGAAAGATA	TTAAAATATT	TGCGCAGACAA	AATATTGTTG	CTACTCCACG
301	AGACTATAAT	GAAGAAGATT	TTAAAGTTAT	TGCAAGAAAA	GAAGTATTTT
351	CAACTGGACT	AATGATGAA	CTTATTGACA	AATGCTTAGT	TGAACTTCTT
401	TCATCAAGCG	ATGTTTCAGA	TAGACAAAAAA	CTTCAATGAT	TTGGATTTCA
451	ACTTAAGGGA	AATCAATTAG	CAAAGACCCA	TTTATTAACA	GCTCTTCAA
501	CTCAAAAGCA	GTATTTCTTT	CAAGACGAAT	GGAACCAAGT	TAGAGCAATG
551	ATTGGAAATG	AGCTCTTCCG	ACATCTCTAC	ACTAAATATT	TAATATTCCA
601	GCGAACTTCT	GAAGGAACTC	TTGTTCAATT	TTGCGGGAAAT	AACGTTTTG
651	ATCATTGAA	AGTCAACGAT	AAGTTGACA	AAAAGCAAAA	AGGTGGAGCA
701	GCAGACATGA	ATGAACCTCG	ATGTTGATCA	ACCTGCAAAT	ACAATGTCAA
751	GAATGAGAAA	GATCACTTT	TCAACAAACAT	CAACGTGCCG	AATTGGAATA
801	ATATGAAATC	AAGAACCGAGA	ATATTTTATT	GCACTCATT	TAATAGAAAT
851	AACCAATTCT	TCAAAAAGCA	TGAGTTTGTG	AGTAACAAAAA	ACAATATTTC
901	AGCGATGGAC	AGAGCTCAGA	CGATATTACAC	GAATATATTCA	AGATTTAATA
951	GAATTAGAAA	GAAGCTAAAAA	GATAAGGTTA	TCGAAAAAAT	TGCCTACATG
1001	CTTGAGAAG	TCAAAGATT	TAACCTAAC	TACTATTTAA	CAAAATCTTG
1051	TCCTCTTCCA	GAAAATTGGC	GGGAACGGAA	ACAAAAAAATC	GAAAACCTGA
1101	TAAATAAAAC	TAGAGAAGAA	AAGTCGAAGT	ACTATGAAGA	GCTGTTAGC
1151	TACACAACCTG	ATAATAAATG	CGTCACACAA	TTTATTAATG	AATTTTCTA
1201	CAATTACCTC	CCCAAAGACT	TTTGACTGG	AAGAAACCGT	AAGAATTTTC
1251	AAAAGAAAGT	TAAGAAATAT	GTGGAACCTAA	ACAAGCATGA	ACTCATTCA
1301	AAAAACTTAT	TGCTTGAGAA	GATCAATACA	AGAGAAATAT	CATGGATGCA
1351	GGTTGAGACC	TCTGCAAAGC	ATTTTTATTA	TTTGATCAC	GAAAACATCT
1401	ACGTCTTATG	GAAATTGCTC	CGATGGATAT	TCGAGGATCT	CGTCGTCTG
1451	CTGATTAGAT	GATTTTCTA	TGTCACCGAG	CAACAGAAAA	GTTACTCCAA
1501	AACCTATTAC	TACAGAAAAGA	ATATTTGGGA	CGTCATTATG	AAAATGTCAA
1551	TCGCAGACTT	AAAGAAGGAA	ACGCTTGCTG	AGGTCCAAGA	AAAAGAGGTT
1601	GAAGAATGGA	AAAAGTCGCT	TGGATTTGCA	CCTGGAAAAC	TCAGACTAAT
1651	ACCGAAGAAA	ACTACTTTCC	GTCCAATTAT	GACTTTCAAT	AAGAAGATTG
1701	TAAATTTCAGA	CCGGAAGACT	ACAAAATTAA	CTACAAATAC	GAAGTTATTG
1751	AACTCTCACT	TAATGCTTAA	GACATTGAG	AATAGAATGT	TTAAAGATCC
1801	TTTTGGATTTC	GCTGTTTTA	ACTATGATGA	TGTAATGAAA	AAGTATGAGG
1851	AGTTGTTTG	CAAATGGAAG	CAAGTTGGAC	AACCAAAACT	CTTCTTTGCA
1901	ACTATGGATA	TCGAAAAGTG	ATATGATAGT	GTAAACAGAG	AAAAACTATC
1951	AACATTCTA	AAAACTACTA	AATTACTTTC	TTCAGATTT	TGGATTATGA
2001	CTGCACAAAT	TCTAAAGAGA	AAGAATAACA	TAGTTATCGA	TTCGAAAAAC
2051	TTTAGAAAGA	AAGAAATGAA	AGATTATTTT	AGACAGAAAT	TCCAGAAGAT
2101	TGCACTTGA	GGAGGACAAT	ATCCAACCTT	ATTCACTGTT	CTTGAAAATG
2151	AACAAAATGA	CTTAAATGCA	AAGAAAACAT	TAATTGTTGA	AGCAAAGCAA
2201	AGAAATTATT	TTAAGAAAGA	TAACCTTACTT	CAACCAGTCA	TTAATATTG
2251	CCAATATAAT	TACATTAAC	TTAATGGGAA	GTTTATAAAA	CAAACAAAAG
2301	GAATTCCCTCA	AGGTCTTGA	GTTCATCAA	TTTGTCTAC	ATTTTATTAT
2351	GCAACATTAG	AGGAAAGCTC	CTTAGGATTC	CTTAGAGATG	AATCAATGAA

FIG. 9A



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2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
 2451 TTTTGATTAC AACTCAAGAG ATAATGCAG TATTGTTTAT TGAGAAACTT
 2501 ATAAACGTAA GTCGTGAAAA TGGAATTTAAA TTCAATATGA AGAAACTACA
 2551 GACTAGTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
 2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
 2651 TCAATTGATA TGAAAACCTCT TGCTTTAATG CCAAATATTAA ACTTGAGAAT
 2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
 2751 CAATGTTGGCT CAAGAAGAAA CTAAAGTCGT TTTAATGAA TAACATTACC
 2801 CATTATTTA GAAAGACGAT TACAACCGAA GACTTGCAG ATAAAACCTCT
 2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
 2901 AATACAAGGA CCACCTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC
 2951 TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
 3001 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
 3051 ACTTTTCCT TAGCACACTG AAGCACTTAA TTGAAATATT CAGCACAAAA
 3101 AAGTACATT TCAACAGAGT TTGCATGATC CTCAGGCAA AAGAAGCAAA
 3151 GCTAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
 3201 CTATTCTAAC TTATTTGGG AAGTTAATT TCAATTTTG TCTTATATAC
 3251 TGGGGTTTTG GGGTTTGGG GTTTTGGGG

FIG. 9B

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
 51 LEDIKIFQAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
 101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
 151 IGNELFRHLY TKYLIQFRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA
 201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVW NWNNMKSRTTR IFYCTHFNRN
 251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAM
 301 LEKVKDFNFN YYLTKSCPPL ENWRERKQKI ENLINKTREE KSKYYEELFS
 351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHIELH
 401 KNLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKL RWIFEDLVVS
 451 LIRCFFYVTE QQKSYSKTY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
 501 EEWKKSLGFA PGKLRLIPKK TTFRPIMTFN KIVIVNSDRKT TKLTTNTKLL
 551 NSHMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA
 601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN
 651 FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLLIVEAKQ
 701 RNYFKKDNLQ QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFY
 751 ATLEESSLGF LRDESMNPEN PNVNLLMRLL DDYLLITTQE NNAVLFIEKL
 801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
 851 SIDMKTALM PNINLRIEGI LCTLNLMQT KKASMWLKKK LKSFLMNNIT
 901 HYFRKTITTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMID
 951 LEVSKIISV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
 1001 KYIFNRVCMI LKAKEAKLKS DQCQSLIQYD A

FIG. 10



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1 CCCCCAAAACCCAAAACCCCTATAAAAAGAAAAATTGAGGTAGTTAGA 60
 1 GGGGTTTGGGGTTTGGGGATATTTTTCTTTAATCCATCAAATCT

 a P Q N P K T P K P L * K K K K L R * F R -
 b P K T P K P Q N P Y K K R K N * G S L E -
 c P K P Q N P K T P I K K E K I E V V * K -

 61 AATAAAAATATTATTCCCGCACAAATGGAGATGGATATTGATTTGGATGATAGAAAATT 120
 61 TTATTTTATAATAAGGGCGTGTACCTACCTATAACTAAACCTACTATATCTTTAA

 a N K I L F P H K W R W I L I W M I * K I -
 b I K Y Y S R T N G D G Y * F G * Y R K F -
 c * N I I P A Q M E M D I D L D D I E N L -

 TACTTCCTAATACATTCAACAAGTATAGCAGCTTTGAGTACAAGAAAGGATGCAAAA 180
 121 ATGAAGGATTATGTAAGTTGTCATATCGTCGAGAACATCACTGTTCTTCCTACGTTT

 a Y F L I H S T S I A A L V V T R K D A K -
 b T S * Y I Q Q V * Q L L * * Q E R M Q N -
 c L P N T F N K Y S S S C S D K K G C K T -

 CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCAAAGTTGCAAAAACAATTAG 240
 181 GTAACTTTAGACCGAGCTTAGCGGAAGTAACTGATAAGGTTCAACGTTTTGTTAATC

 a H * N L A R N R L H * L F Q S C K N N * -
 b I E I W L E I A F I D Y S K V A K T I R -
 c L K S G S K S P S L T I P K L Q K Q L E -

 AGTTCTACTTCTCGGATGCAAATCTTATAACGATTCTTCTTGAGAAAATTAGTTAA 300
 241 TCAAGATGAAGAGCCTACGTTAGAAATATTGCTAAGAAAGAACTCTTTAATCAAATT

 a S S T S R M Q I F I T I L S * E N * F * -
 b V L L L G C K S L * R F F L E K I S F K -
 c F Y F S D A N L Y N D S F L R K L V L K -

 AAAGCGGAGAGCAAAGAGTAGAAATTGAAACATTACTAATGTTAAATAAATCAGGTAA 360
 301 TTTCGCCTCTCGTTCTCATCTTAACTTTGTAATGATTACAAATTATTTAGTCCATT

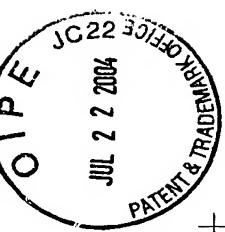
 a K A E S K E * K L K H Y * C L N K I R * -
 b K R R A K S R N * N I T N V * I K S G N -
 c S G E Q R V E I E T L L M F K * N Q V M -

 TGAGGATTATTCTATTTTAGATCACTCTTAAGGAGCATTATGGAGAAAATTACTTAA 420
 361 ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCCTCGTAATACCTCTTTAATGAATT

 a * G L F Y F L D H F L R S I M E K I T * -
 b E D Y S I F * I T S * G A L W R K L L N -
 c R I I L F F R S L L K E H Y G E N Y L I -

FIG. 12A

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TACTAAAAGGTAAACAGTTGGATTATTCCTAGCCAACAATGATGAGTATATTAAATT
 421 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
 ATGATTTCCTTCAAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTAA

 a Y * K V N S L D Y F P S Q Q * * V Y * I -
 b T K R * T V W I I S L A N N D E Y I K F -
 c L K G K Q F G L F P * P T M M S I L N S -

 CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT
 481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
 GTATACTCTTACTCAGTTCTAGAGCTATGTTAGTCTGAATGGTTCTGTTGAGCGATA

 a H M R M S Q R I S I H Q T Y Q R Q T R Y -
 b I * E * V K G S R Y I R L T K D K L A I -
 c Y E N E S K D L D T S D L P K T N S L * -

 AAAACGCAAGAAAAGTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTG
 541 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
 TTTTGCCTTCTTTCAAACATTAGCTTGTCTCTGAATAACGTAATGATAAGC

 a K T Q E K V * * S N S R R T Y C I Y Y S -
 b K R K K K F D N R T A E E L I A F T I R -
 c N A R K S L I I E Q Q K N L L H L L F V -

 TATGGGTTTATTACAATTGTTTAGGTATCGACGGTGAACCTCCGAGTCTTGAGACAAT
 601 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
 ATACCCAAAATAATGTTAACAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA

 a Y G F Y Y N C F R Y R R * T P E S * D N -
 b M G F I T I V L G I D G E L P S L E T I -
 c W V L L Q L F * V S T V N S R V L R Q L -

 TGAAAAAGCTGTTACAACCTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT
 661 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
 ACTTTTCTGACAAATGTTGACTTCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA

 a * K S C L Q L K E S Q F * K F * C V C H -
 b E K A V Y N * R N R S S E S S D V Y A I -
 c K K L F T T E G I A V L K V L M C M P L -

 TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTAAATGGATAGCTATAGAAACAAA
 721 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 780
 ATAAAACACTTAATTAGAGTTATAGAATAGAGTTAAATTACCTATCGATATCTTGT

 a Y F V N * S Q I S Y L N L M D S Y R N K -
 b I L * I N L K Y L I S I * W I A I E T N -
 c F C E L I S N I L S Q F N G * L * K Q T -

 CCAAATAAACCATGCAAGTTAATGAAATACGTTAAATCCTTGGGACAAATGCACAC
 781 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 840
 GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTAGGAAACCTGTTACGTGTG

 a P N K P C K F N G I Y V K S F G T N A H -
 b Q I N H A S L M E Y T L N P L G Q M H T -
 c K * T M Q V * W N I R * I L W D K C T L -

 TGAATTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTAGC
 841 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
 ACTTAAATATAACCTAACGAAATTCTGTTATCTGTTACGAAATCTCTGACTAAATCG

 a * I Y I G F L K H R Y T E C F R D * F S -
 b E F I L D S * S I D T Q N A L E T D L A -
 c N L Y W I L K A * I H R M L * R L I * L -

FIG. 12B

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TTACAACAGATTACCTGTTTGATTACTCTGCTCATCTCTTATATCTTAAAGAAGCA
 901 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 960
 AATGTTGTCTAATGGACAAAACAAATGAGAACGAGTAGAGAATATAGAAATTCTCGT

a L Q Q I T C F D Y S C S S L I S L K E A -
 b Y N R L P V L I T L A H L L Y L * K K Q -
 c T T D Y L F * L L L L I S Y I F K R S R -

GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTCAAAATTGTTGATTCTTCTGTAACC
 961 -----+-----+-----+-----+-----+-----+-----+-----+ 1020
 CCGCTTTACTTTCTTCTGATTCTTCTAAAGTTAAACAACATAAGAACATTGG

a G E M K R R L K K E I S K F V D S S V T -
 b A K * K E D * R K R F Q N L L I L L * P -
 c R N E K K T K E R D F K I C * F F C N R -

GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAACGAGCTATCACAAATCCTGATTG
 1021 -----+-----+-----+-----+-----+-----+-----+-----+ 1080
 CCTTAATTGTTGTTCTTATAATCGTTGCTTTCTTCTCGATAGTGTAGGACTAAG

a G I N N K N I S N E K E E E L S Q S * F -
 b E L T T R I L A T K K K K S Y H N P D S -
 c N * Q Q E Y * Q R K R R R A I T I L I L -

TTAAAGATTCAAAAATTCCAGGTAAAGAGAGATACTTCATTAAATTCAATATATTATAG
 1081 -----+-----+-----+-----+-----+-----+-----+-----+ 1140
 AATTCTAAAGTTTAAGGTCCATTCTCTATGTAAGTAATTAAAGTATATAATATC

a L K I S K I P G K R D T F I K I H I L * -
 b * R F Q K F Q V R E I H S L K F I Y Y S -
 c K D F K N S R * E R Y I H * N S Y I I V -

TTTTTCATTCACAGCTGTTATTTCTTTATCTTAACAATATTTTGATTAGCTGGAA
 1141 -----+-----+-----+-----+-----+-----+-----+-----+ 1200
 AAAAGTAAAGTGTGACAATAAAAGAAAATAGAATTGTTATAAAAACATAATCGACCTT

a F F I S Q L L F S F I L T I F F D * L E -
 b F S F H S C Y F L L S * Q Y F L I S W K -
 c F H F T A V I F F Y L N N I F * L A G S -

GTAAAAAGTATCAAATAAGAGAACGCTAGACTGAGGTAACCTAGCTTATTCACATTCA
 1201 -----+-----+-----+-----+-----+-----+-----+-----+ 1260
 CATTTTCATAGTTATTCTCTCGCGATCTGACTCCATTGAATCGAATAAGTGTAGTA

a V K S I K * E K R * T E V T * L I H I H -
 b * K V S N K R S A R L R * L S L F T F I -
 c K K Y Q I R E A L D * G N L A Y S H S * -

AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTAAAAA
 1261 -----+-----+-----+-----+-----+-----+-----+-----+ 1320
 TCTAGCTGGAAGTATAGTTATGCTACTATTCCCTTGTGTCAGTAGGCAAATT

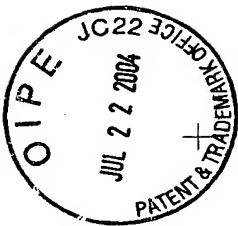
a R S T F I Y P I R * * G N S S H P F * K -
 b D R P S Y I Q Y D D K E T A V I R F K N -
 c I D L H I S N T M I R K Q Q S S V L K I -

TAGTGCTATGAGGACTAAATTAGAGTCAGAAATGGAGGCCAAATCTTAATCAAAA
 1321 -----+-----+-----+-----+-----+-----+-----+-----+ 1380
 ATCACGATACTCCTGATTAAACATCTAGTTACCTCGGCTTTAGAATTAGTTT

a * C Y E D * I F R V K K W S R N L N Q K -
 b S A M R T K F L E S R N G A E I L I K K -
 c V L * G L N F * S Q E M E P K S * S K R -

FIG. 12C

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GAATTGCGTCGATATTGCAAAAGAACATCGAACTCTAAATCTTCGTTAATAAGTATTACCA
 1381 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1440
 CTTAACGCGACTATAACGTTTCTTAGCTTGAGATTAGAAAGCAATTATTCTATAATGGT

a E L R R Y C K R I E L * I F R * * V L P -
 b N C V D I A K E S N S K S F V N K Y Y Q -
 c I A S I L Q K N R T L N L S L I S I T N -

ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA
 1441 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1500
 TAGAACTAACTAACTTCTCTAACTGCTCCGTTGACGTGCTTCTAGTAATTCTTTATTT

a I L I D C R D * R G N C T E D H * R N K -
 b S * L I E E I D E A T A Q K I I K E I K -
 c L D * L K R L T R Q L H R R S L K K * S -

GTAACTTTATTAATTAGAGAATAAAACTAAATTACTAATATAGAGATCAGCGATCTCAA
 1501 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1560
 CATTGAAAATAATTAACTCTTATTTGATTAAATGATTATCTCTAGTCGCTAGAAGTT

a V T F I N * R I N * I T N I E I S D L Q -
 b * L L L I R E * T K L L I * R S A I F N -
 c N F Y * L E N K L N Y * Y R D Q R S S I -

TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAATACAAACCTGGTCAAAAT
 1561 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1620
 AACTGCTTATTTGACTTGATTCAATCTGTTATTTTATGTTGAAACCAGTTA

a L T K * K L N * S * T I K N T N L G Q N -
 b * R N K S * T K V R Q * K I Q T L V K I -
 c D E I K A E L K L D N K K Y K P W S K Y -

ATTGAGGAAGGAAAAGAACAGCTTAGCAAAAGAAAAATAAGCAATAAAATAATGA
 1621 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1680
 TAACTCCTCCTTCTGGTCAATCGTTCTTTTATTCCGTATTTACT

a I E E G K E D Q L A K E K I R Q * I K * -
 b L R K E K K T S * Q K K K * G N K * N E -
 c * G R K R R P V S K R K N K A I N K M S -

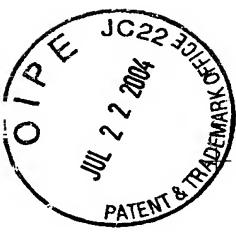
GTACAGAAAGTGAAGAAATAAAAGATTATTTTTCAATAATTATTGAAAAGAGGGTT
 1681 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1740
 CATGTCTTCACTCTTATTTCTAAATAAAAAGTTATTAAATAACTTTCTCCCCAA

a V Q K * R N K R F I F F N N L L K R G V -
 b Y R S E E I K D L F F S I I Y * K E G F -
 c T E V K K * K I Y F F Q * F I E K R G F -

TTGGGGTTTGGGGTTTGGGG
 1741 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1762
 AACCCCAAAACCCCAAAACCC

a L G F W G F G -
 b W G F G V L G -
 c G V L G F W -

FIG. 12D



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2	EVDVQNQADNHGIIHSALKTCEEIKEAKTLYSWIQKVRICRNRQSOSHYKDL	51
19	ELELEMQENQNDIQVRVK....IDDPKQY..LVNVTAACLLQEGSYQQDK	62
52	EDIKIFQAQTNIVATPRDYNEEDFKVIARKEVF..STGLMIELIDKCLVELL	100
63	DERRYIITKALL....EVAESDPFICQLAVYIRNELYIRTTNYIVAF.	107
101	SSSDVSDRQKLQCFGQLKGNQLAKTHLLTALSTQKQYFFQDEWNQVRAM	150
108CVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYI	144
151	IGNELFRHLYTKYLIFQRTSEGTIVQFCGNVNFDHVKVNDKFDDKKQKGGA	200
145	FDATEOFKNLY.....LDRILSQDIRKELTFRKCLQRQCVRSKF	181
201	ADMNE...PRCCSTCKYNVKNEKDHFLLNNINVPNWNNMKSRTTRIFYCTHF	247
182	SEFNEYQLGKYCTES..QRKKTMFRLSVTNKQKWDQTKKK.....	220
248	NRNNQFFKKHEFVSNKNNISAMDRAQTIFTNIFRFNRIRKKLKDVKIEKI	297
221	..RKENLLTKLQAIKESEDKSKRETG.....DIMNVEDAIIKALKPAVMKKI	264
298	AYMLEKVKDGFNFNYYLTKSCPLPENWRERKQKIEALKTREESKYYEE	347
265	AKRQNAMK.....KHMKAPKIPNSTLESKYLTFKD	294
348	LFSYTTDNKCVTQFINEFFYNILPKDFLTGRNRKNFQKKVKKYVELNKH	397
295	LIKFCHISEP.....KERVYKILGKKYPKTEEEYKAAGFDSASAPFN.PE	338
398	LIHKNLLLEKINTREISWMQVETSACKHFYYFDHENIYVWLKLLRWIFEDL	447
339	LAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSN..	386
448	VVSLIRCFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKKETLAEVQE	497
387ILKAGVSD.....	394
498	KEVEEWKSLGFAPGKLRLIPKKTTFRPIMTFNKKIVNSDRKTTKLTNT	547
395TTHS	398
548	KLLNSHMLKTLKNRMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL	597
399	IVINK.....ICEPKAVENSKM	415
598	FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNNIVID	647
416	F..PLQFFSAIEAVN.EAVTKGFKAKK..RENMLNKGQIEAVKE..VVE	457
648	SKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKTLIVE	697
458	KTDEEKKDM.....ELEQTEEGEFVKVNEGIGKQYINSIELAIK	496
698	AKQRNYFKKDNLLOPVINICQYNYINFNGKFYQTKGIPQGLCVSSILSS	747
497	IAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGL	546
748	FYYATLEESSLGFLRDESMNPENPNVNLMLRLTDYLLITTOENNANLFI	797
547	MVKORCEKSSFYIESSPSSOCNKCYLEVDL.....	576

FIG. 13A



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798 EKLINVSRENGFKFNMKK. LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD 846
 577PGDELRPSMQKLLQEKGKLGGG..TDFPYECIDEWTKNKTHVD 617
 847 WIGISIDMKTALMPNIHLRIEGILCTLNLNMQTKKASMWLKKLKSFLM 896
 618 NIVILSDMMIAEGYSINVRGSSIVNSI.....KKYKDEVN 653
 897 NNITHYFRKTITTEDFANKTLNKLFISSGGYKYMCAKEYKD.HFKKNLAM 945
 654 PNIKIF...AVDLEGYG.....KCLNLGDEFNENNYIKIFGM 687
 946 SSMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIE 995
 688 SDSI.....LKFISAKQGGA.....NMVE 706
 996 IFSTKKYIFNRVC 1008
 707 VI..KNFALQKIG 717

FIG. 13B

132 LSTQKQYFFQDEWNQVRAMIGNEL.FRHLYTGYLIFQRTSE..GTLVQFC 178
 1 MSRRNQ.....KKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQI 43
 179 GNNVFDHLKVNDKFDKKQKGGAADMNEPRCCSTCKYNVKNKEHDHFLNNIN 228
 44 KEEDLKLLKFKNQDQDGNSGNDDDEE.....NNSNKQQELLRRVN 84
 229 VPNWNNMKSRTTRIFYCTHFNRRNQFFKKHEFVSNKNNISAMDRAQTIFTN 278
 85QIKQQVQLIKK...VGSKVEKDLNLNEDENKKN 114
 279 IFRFNRIRKKLKDVKIEKIAYMLEVKDFNFNYYLTKSCPLPENWRERKQ 328
 115 GLSEQQVKEEQLRTITEEQVKYQNLVFNMHDYQLDLNESGGHRRRRTDY 164
 329 KIENLINKTREEKSYYEELFSYTTDNKCVTQFINE.FFYNILPKDFLTG 377
 165 DTEKWFEISHDQK.....NYVSIYANQKTSYCWWLKDYFNK 200
 378 RNRKNFQKKVKKYVELNKHELIKNLLKINTREISWMQVETSAKHFYY 427
 201 NNYDHLNVSINRLE..TEAEFYAFDDFSQTIKLTNNNSYQTVNID..... 242
 428 FDHENIYVLWKLLRWI..FEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNI 475
 243 VNFDDNNLCILALLRFLLSLERFNILNIRSSY..TRNQYNFEKIGELLETI 290
 476 WDViMKMSIADLKETLAEVQEKEVEEWKKSLGFAPGKLRLIPKKTTFRP 525
 291 FAVVFSHR.....HLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQ 330
 526 IMTFNKKIVNSDRKTTKLTNTKLLNSHMLKTLKNRMFKDPFGFAVFNY 575
 331 VYSFSTDLKLV..TNKVQDYFKFLQEFPLRTHVSQQAIPVSATNAVENL 378

FIG. 14A

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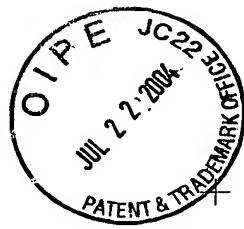
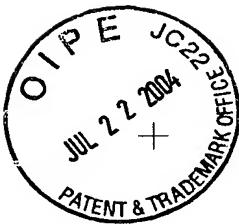


FIG. 14B

FIG. 15



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1	MEMDIDLDDIENL.....LPNTFNKYSSSCSDKGCKTLKSGSKSPS...	42
491	IELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMGGAKKYGSVRTCLEC	540
43	.LTIPKLQKQ.....LEFYFSDANLYNDSFLRKVLKSGEQRVEIETLL	85
541	ALVLGLMVQRCEKSSFYIFSSPSSQCNKCYL.EVDLPGDELRPSMQKLL	589

FIG. 16

telomerase p43	LQK[REDACTED]LEFYFSDANLYNDSFLRKVLKSGEQRVEIETLLM
human La	ICHQ[REDACTED]UEYYFGDFNLPRDKFLKEQI.KLDEGWVPLEIMIK
Xenopus La	ICE[REDACTED]PIEYYFGDHNLPRDKFLKQQI.LLDDGWVPLETMIK
Drosophila La	ILR[REDACTED]OVEYYFGDANLNRDKFIREQIGKNEDGWVPLSVLVT
S. c. Lhplp	CLK[REDACTED]QVEFYFSEFNFPYDRFLRTTAEK.NDGWVPISTIAT

FIG. 18

1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
 61 tagatttaat ttagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
 121 gccaaaagcc gaaaaattgt ggtggact tgaatttagag atgcaagaaa accaaaatga
 181 tataataattt agggtaaga ttgacgtcc taagcaat ctcgtgaacg tcactgcagc
 241 atgtttgtg taggaaggta gttactacta agataaaatg gaaagaagat atatcatcac
 301 taaagcactt cttgaggtgg ctgagtcga tcctgagttc atctgctagt tggcagtcta
 361 catccgtaat gaactttaca tcagaactac cactaactac attgttagcat ttttgttgt
 421 ccacaagaat actcaaccat tcacgtaaaa gtacttcaac aaagcagttac tttgcctaa
 481 tgacttactg gaagtctgtg aatttgcata ggttctctat atttttgtg caactgaatt
 541 caaaattt tatcttgata ggatacttc ataagatatt cgtaaggaaac tcacttccg
 601 taagtgtta caaagatgcg tcagaagcaa gttttctgaa ttcaacaaat actaacttgg
 661 taagtattgc actgaatcct aacgtaaagaa aacaaatgttc cgttacccct cagttaccaa
 721 caagtaaaag tgggattaaa ctaagaagaa gggaaaagag aatctctaa ccaaacttta
 781 ggcataaaag gaatctgaag ataagtccaa gagagaaact ggagacataa tgaacgttga
 841 agatgcatac aaggctttaa aaccagcagt tatgaagaaa atagccaaag gatagaatgc
 901 catgaagaaa cacatgaagg cacctaaat tcctaactct accttggaaat caaagtactt
 961 gaccccttcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa
 1021 gatcccttggt aaaaaatacc ctaacccga agaggaatac aaagcgcct ttggtgattc
 1081 tgcacatcgca cccttcaatc ctgatattgc tgaaaaagcgat atgaagattt aatctctaa
 1141 aacatggaa aatgaactca gtgaaaagg caacactgct gaggttggg ataatttaat
 1201 ttcaagcaat taactcccat atatggccat gttacgttaac ttgtctaaaca tcttaaaagc
 1261 cggtgtttca gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt
 1321 tgagaactcc aagatgttcc ctcttcaatt ctttagtgc attgaagctg ttaatgaagc
 1381 agttacttaag ggatcaagg ccaagaagag agaaaaatatg aatcttaaag gtcaaatcgaa
 1441 agcagtaaaag gaagttgtg aaaaaacccgaa tgaagagaag aaagatattgg agttggagat
 1501 aaccgaagaa ggagaatttg tttaaggtaa cgaaggaaat ggcaggaaat acattaactc
 1561 cattgaactt gcaatcaaga tagcgttaa caagaattta gatgaaatca aaggacacac
 1621 tgcaatcttc tctgtatgtt ctggttctat ggtacctca atgtcagggtg gagccaagaa
 1681 gtatggttcc gttcgtactt gtctcgatgt tgcatttagt cttgggttga tggtaaaata
 1741 acgttgtgaa aagtccatc tctacatctt cagttcacct agttctcaat gcaataagtg
 1801 ttacttagaa gttgatctcc ctggagacga actccgtct tctatgtaaa aacttttgca
 1861 agaaaaagg aaactctgtg gtgtactga tttccctat ggtgcattt atgaatggac
 1921 aaagaataaa actcacatcg acaatatcg tattttgtct gatatgatga ttgcagaagg
 1981 atattcagat atcaatgtta gaggcaggcc tattgttaac agcataaaa agtacaagga
 2041 tgaagtaaat cctaacatta aaatcttgc agttgactta gaagggtacg gaaagtgcct
 2101 taatcttaggt gatgagttca atgaaaacaa ctacatcaag atattcggtt tgagcgattc
 2161 aatcttaaag ttcatatccag ccaagcaagg aggagcaat atggtgcag ttatcaaaaa
 2221 ctttggccctt caaaaaatag gacaaaatgt agttcttgc gattcttcta taacaaaaat
 2281 ctcaccccccac tttttgttt tatttgcattag ccattatgaa atttaaattt ttatcttattt
 2341 atttaagttt cttacatagt ttatgtatcg cagttatgaa gccttattcaa atgattctgc
 2401 aaagaacaaa aaagattaaa a

FIG. 19

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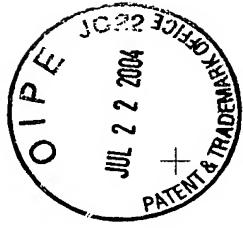


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	Motif A	Motif B	Motif C	Motif D	Motif E
Consensus telomerase p123	h--hDh---h--h	h---+ -QG---SP	h--YhDhhhh	Gh-h---K	h-hLgh-h
Dong (LINE)	GOPLKFFATMDIEKCYDSVANREKLSTFLKTTKLL-100-KFYKQTKGIFQGLCVSSILSSFYATLEESSLGL	KNRNLHCTYDDYKKAFTSIPHSMWLIQVLEIYKIN- 28-RQIAIKKGIYQGDSLSPLWFCLALNPFLSHQLHNDR			
a1 S.c. (groupII)	FGGSNWFREVDLKKCFDTISHDLIIKEKLKRYISD- 26-HVPVGPRLVCQOGAPTSPALCNAVLLRLDRRLAGLA	LKKKKSVTVDYGDAYFSPVPLIDEDFRKYTAFTIP- 7-GIRYQYNVLFQGMKGSSPAIFOSSMTKILLEPFRQN			
HIV-RT	VLEPELYFMKFDVKSCYDSIPRMECMILKDALKN- 68-KCYIREDGLFQGSSLSAPIVDLVYDLLFEFYSEFK	VLEPELYFMKFDVKSCYDSIPRMECMILKDALKN- 68-KCYIREDGLFQGSSLSAPIVDLVYDLLFEFYSEFK			
L8543.12					

FIG. 17

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MEIENNOAQOPKAELWWELELEMQENQNDIQVRVKIDDPKQYL
 VNVTAACLLQEGSYYQDKDERRIITKALLEVAESDPEFICQLA
 VYIRNELYIRTTTNYIVAFCVVHKNTQPFIEKYFNKAVLLPNDL
 LEVCEFAQVLYIFDATEFKNLYLDRILSQDIRKELTFRKCLQRC
 VRSKFSEFNEYQLGKYCTESQRKKTMFRLSVTNKQKWDQTKKK
 RKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKI
 AKRQNAMKKHMKAPKIPNSTLESKYLTFKDLIKFCHISEPKERV
 YKILGKKYKPTEEYKAAGDSASAPFNPAGKRMKIEISKTW
 ENELSAKGNTAEVWDNLISSNQLPYMAMILRNLNSILKAGVSDTT
 HSIVINKICEPKAVENSKMFPLOFFSAIEAVNEAVTKGFKAKKR
 ENMNLLKGQIEAVKEVVEKTDEKKDMELEQTEEGEFVKVNEGIG
 KQYINSIELAIIKAVNKLDEIKHTAIFSDVSGSMSTSMSGGA
 KKYGSVRTCLECALVLGLMVQRCEKSSYIFSSPSSQCNKCYL
 EVDLPGDELPRSMQKLLQEKGLGGTDFPYECIDEWTKNKTHV
 DNIVILSDMMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFA
 VDLEGYKGCLNLGDEFNENNYIKIFGMSDSILKFISAKQGGANM
 VEVIKNFALQKIGQK

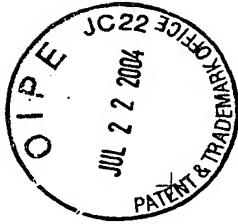
FIG. 20

MSRRNQKKPQAPIGNETNLDVQLQNLEVYKSQIEHYKTQQQQIK
 EEDLKLLFKNQDQDGNSGNDDDEENNSNKKQELLRRVNQIKQ
 QVQLIKKVGSKVEKDLNLNEDENKKNGLSEQQVKEEQLRTITEE
 QVKYQNLVFNMDYQLDLNESGGHRRRRETDYDTEKWFEISHDQ
 KNYVSIYANQKTSYCWLKDYFNKNNDHNLVSINRLETEAEFY
 AFDDFSQTIKLTLNNSYQTVNIDVNFDNNLICILALLRFLLSLERF
 NILNIRSSYTRNQYNEKIGELLETIFAVVFSHRLQGIHLQVP
 CEAHQYLVNSSSQISVFKDSQLQVYSFSTDLKLVDTNKVQDYFKF
 LQEFPRLTHVSQQAIPVSATNAVENLNVLKKVKHANLNVLVSIP
 TQFNFDYFVNQHQLKLEFGLPNIILTQKLENLLSIKQSKNL
 KFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNQEETPETKD
 ETPSESTSGMKFFDHLSELTELEDFSVNLQATQEIYDSLHKLLI
 RSTNLKKFKLSYKYEIMEKSKMDTFIDLKNIYETLNMLKRCVNI
 SNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFN
 NVKSAKIESSSLESLEDISLCKSIAASKNLQNVNIIASLLYPN
 NIQKNPFNKPNLFFKQFEQLKNLENVSINCILDQHILNSISEF
 LEKNKKIKAFLKRYYLLQYYLDYTKLFKTLQQLPELNQVYINQ
 QLEELTVSEVHKQWENHKQKAFYEPLCEFIKESSTQLQLIDFD
 QNTVSDDSIKKILESISESKYHYLRLNPSQSSSLIKSENEEIQ
 ELLKACDEKGVLVKAYYKFPLCLPTGTYYDNSDRW

FIG. 22

MKILFEFIQDKLDIDLQTNSTYKENLKGHFNGLDEILTTCFAL
 PNSRKIALPCLPGDLSHKAVIDHCIYLLTGELYNNVLTFGYKI
 ARNEDVNNSLFCHSANVNVTLLKGAAWKMFHSLVGTYAFVDLI
 NYTVIQNGOFFTQIVGNRCNEPHLPPKWKVRSSSSATAAQIK
 QLTERPVTKQFLHKLNNINSSSSFPYSKILPSSSIKKLTLREA
 IFPTNLVKIPQRLKVRINLTLQKLLKRHKRLNYVSILNSICPL
 EGTVLDSLHLSRQSPKERVLKFIIIVILQKLLPQEMFGSKKNKGK
 IIKNLNLSSLPLNGYLPFDSSLKLRKDFRWLFIISDIWFTKH
 NFENLNQLAICFISWLRQPKIIQTFYCTEISSTVTIVYFR
 HDTWNKLITPFIVEYFKTYLVEENNVRNHSYTLSNPNHSKMRI
 IPKKSNNEFRIIAIPCRGADEEEFTIYKENHNAIQPTQKILEY
 LRNKRPTSTKIYSPTQIADRIKEFKQRLKKFNNVLPELYFMK
 FDVKSCYDSIPRMEMCRILKDALKNENGFFVRSQYFFNTNTGVL
 KLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFKTA
 LWVEDKCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS
 QDTLILKLAADDFLIISTDQQQVINIKKLMGGFQKYNAKANRDK
 ILAVSSQSDDDTVIQFCAMHIFVKELEVWKSSTMNFHIRSKS
 SKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISE
 CYKSAFKDLSINVTONMQFHSFLQRIIEMTVSGCPITKCDPLIE
 YEVRFTILNGFLESLSSNTSKFKDNIIILRKEIQHLQAYIYIYI
 HIVN

FIG. 23



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FIG. 21



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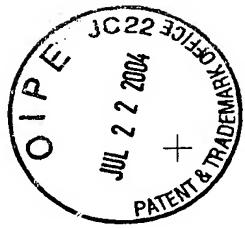
Oxytricha
Eupletes

LCVSYILSSFYANLEENALQFLRKEESMDPEKPETNLLMRLT
LCVSSILSSFYATLEESSLGFLRDESMNPENPNVNLLMRLT

FIG. 24

ATTTATACTCATGAAAATCTTATTGAGTCATTCAAGACAAGCTTGACATTGATCTACA
GACCAACAGTACTTACAAAGAAAATTAAATGTGGTCATTCAATGGCCTCGATGAAAT
TCTAACTACGTGTTCGCACTACCAAAATTCAAGAAAAATAGCATTACCATGCCTTCTGG
TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT
ATACAACAAACGTACTAACATTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAAATAG
TCTTTTTGCCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCCTGCTTGGAAAAT
GTTCCACAGTTGGTCGGTACATACGCATTGTTGATTATTGATCAATTATAACAGTAAT
TCAATTAAATGGGCAGTTTCACTCAAATCGTGGGTAAACAGATGTAACGAACCTCATCT
GCCGCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA
ACTTACAGAACCGAGTACAATAACAAATTCTACACAAGCTCAATATAAATTCCCTTC
TTTTTTCCATTAGCAAGATCCTTCCTCATCATCTATCATAAAAGCTAACTGACTT
GAGAGAAGCTATTTCACAAATTGGTTAAAATTCTCAGAGACTAAAGGTACGAAT
TAATTGACGCTGCAAAGCTATTAAAGAGACATAAGCGTTGAATTACGTTCTATT
GAATAGTATTGCCCACCATGGAAAGGGACCGTATTGGACTTGTGCGATTGAGTAGGCA
ATCACCAAAGGAACGAGTCTTGAATTATCATGGTATTACAGAAGTTATTACCCCA
AGAAATGTTGGCTCAAAGAAAATAAGGAAAATTATCAAGAATCTAAATCTTTATT
AAGTTACCCCTTAAATGGCTATTACCATTTGATAGTTGTTGAAAAAGTTAAGATTAAA
GGATTTCGGTGGTTGTCATTCTGATATTGGTTCACCAAGCACAATTGGAAAACCTT
GAATCAATTGGCGATTGTTCATTCCTGGCTATTAGACAACTAATTCCAAAATTAT
ACAGACTTTTACTGCACCGAAATATCTCTACAGTACAATTGTTACTTAGACA
TGACTTGGAATAAACTTATCACCCCTTATCGTAGAATAATTAAAGACGTACTTAGT
CGAAAACAACGTATGTAGAAACATAATAGTTACACGTTGTCCAATTCAATCATAGCAA
AATGAGGATTATACCAAAAAAGTAATAATGAGTCAGGATTATTGCCATCCCATGCG
AGGGGCAGACGAAGAAGAATTACAATTATAAGGAGAATCACAAAATGCTATCCAGCC
CACTAAAAAATTAGAATACCTAACGAAACAAAAGGCCGACTAGTTTACTAAATATA
TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTAAAGCAGAGACTTTAAAGAAATT
TAATAATGCTTACCAAGAGCTTATTGATGTCAAATCTGCTATGATT
CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGTT
TTTCGTTAGATCTCAATTCTCAATACCAATACAGGTGTATTGAAGTTATTAAATGT
TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
TCATTATCAAATCAGGATGTTAAACGTTGAGAGATGGAATAATTAAACAGCTTT
GTGGGTTGAAGATAAGTGTACATTAGAGAAGATGGCTTTTCAAGGGCTCTAGTTATC
TGCTCCGATCGTTGATTGGGTATGACGATCTTCTGGAGTTTATAGCGAGTTAAAGC
CAGTCCTAGCCAGGACACATTAATTAAACCTGGCTGACGATTCCATTAAATATCAAC
AGACCAAACAGCAAGTGTCAATATCAAAAAGCTTGCCATGGCGGATTCAAAAATATAA
TGCAGAAAGCCAATAGAGACAAAATTAGCCGTAAGCTCCCAATCAGATGATGATACGGT
TATTCAATTGTCAGACATATTGTTAAAGAATTGGAAGTTGAAACATCAAG
CACAAATGAATAATTCCATATCCGTTGAAATCTAGTAAAGGGATATTGCAAGTTAAAT
AGCGCTGTTAACACTAGAAATCTCTATAAAACAATTGACACAAATTAAATTCAACAA
CACCCTCTCATGCAAATTGATCATGTTGAAAGAACATTCCGAATGTTATAAATCTGC
TTTAAGGATCTATCAATTAAATGTTACGCAAAATATGCAATTCTATTGTTCTACAACG
CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTAATCGAGTA
TGAGGTACGATTCAACCATATTGAATGGATTGGAAAGCCTATCTTCAAACACATCAAA
ATTAAAGATAATATCATTCTTTGAGAAAGGAATTCAACACTTGCAAGC

FIG. 26



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human
tez1
EST2
p123

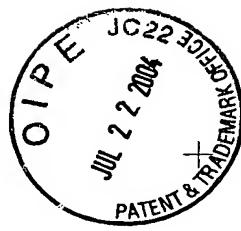
Motif 0
 AKFLHLWLMVVYVLLRSFFYVTEFTFQKNR
 ISEIIEWLVLGGRSNAKMCISDFEKRKQIIFAEFIYWLYNSTIPILOQSFYIITESSDLRNR
 LKDFRWLFISD---IWFTKHNFENINOLAICFISWLFROLIPKIIQTEFYCTEISSTVT-
 TREISWMQVET-SAKHFYYFDHEN-IYVLWKLRLWIFEDLVSLIRCFYVTEQQSKYSK
 * * * * *

human
tez1
EST2
p123

tee1
EST2
p123

FIG. 25

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AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREK
RAERLTSRVKALFSVLNYERA

FIG. 27

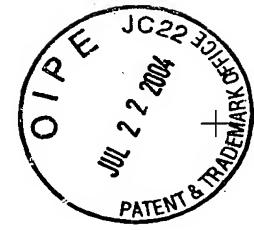
GCCAAAGTTCTGCACGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGGCTTCTTTTCTACCGGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCAGATCGGGAAAGCAGGCCCGCCCTGCTGACGTCAGACTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTAACATGGACTACGTCGTTGGGAGCCAGAACGTTCCGAGAAGAAAGAGGGCAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCCTCAACTACGAGCGGGCGCG

FIG. 28

MTEHHTPKSRLRFLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSVDQTSFSIFLHSTVVG
DSKPDEGVQFSSPKCSQSELIANVVQMFDESFERRNLLMKFSMNHEDFRAMHVNQNDLVSTF
PNYLISILESKNWQLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRKR
TIETSITQNKSARKEVSWNSISISRFSTFYRSSYKKFKQDLYFNLHSICDRNTVHMLQWIFPRQFG
LINAQVKQLHKVPLVSQSTVVPKRLLKVVPLIEQTAKRHLRISLSKVYNHYCPYIDTHDDEKILS
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDETLFLKLSRYESFLHYLMSNIKISEIEWL
VLGKRSNAKMCLSDFEKRQIFAEFIYWLWNSFIIPILQSFYITESSDLRNRTVYFRKDIWKLLCR
PFITSKMEAFEKINEENNVRMDTQKTTLPPAVIRLLPKKNTFRLITNLRKRFLIKMGNSKKMLVSTN
QTLRPVASICLKHLINEESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIJKSCYDRIKQDLM
FRIVKKKLKDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMPFEKVQQLSMSKTSDTLFVDFVDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYQLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKGSVL
LRVVDDEFLFITVNKKDAKKFLNLSLRGFKEHNFSTSLEKTVINFENSNGIINNTFFNESKKRMPFFG
FSVNMRSLDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCN
IYRLGYSMCMRAQAYLKRMDIFIPQRMFITDLLNVIGRKIWKKLAIEILGTYTSRRFLSSAEVKWLFC
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLFHRRRIAD

FIG. 29

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FIG. 30A

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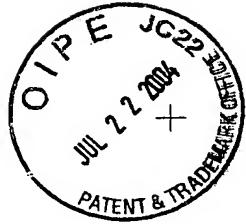
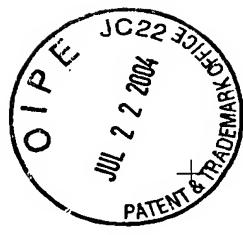


FIG. 30B



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FIG. 31

1



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S-1: FFY VTE TTF QKN RLF FYR KSV WSK
S-2: RQH LKR VQL RDV SEA EVR QHR EA
S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1:	AKF	LHW	LMS	VYV	VEL	LRS	FFY	VTE	TTF	Q
A-2:	LFF	YRK	SVW	SKL	QSI	GIR	QHL	KRV	QLR	DVS
A-3:	PAL	LTS	RLR	FIP	KPD	GLR	PIV	NMD	YVV	

FIG. 32

Poly 4

t t c
 t a a g c c t c g
 5' - c a g a c c a a a g g a a t t c c a t a a g g - 3'
 O T K G I P Q G

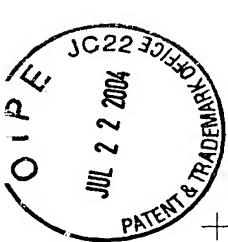
4 (B')

5 (c')

D D Y L L I T
 3' - ctg ctg atg gag gag tag tgg - 5'
 a a a a a a a a
 t t t t
 c c
 Poly 1

FIG. 34

1



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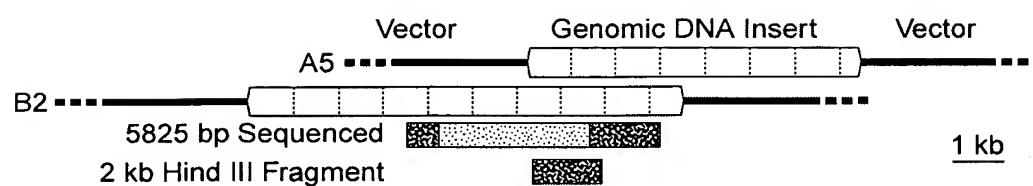


FIG. 33A

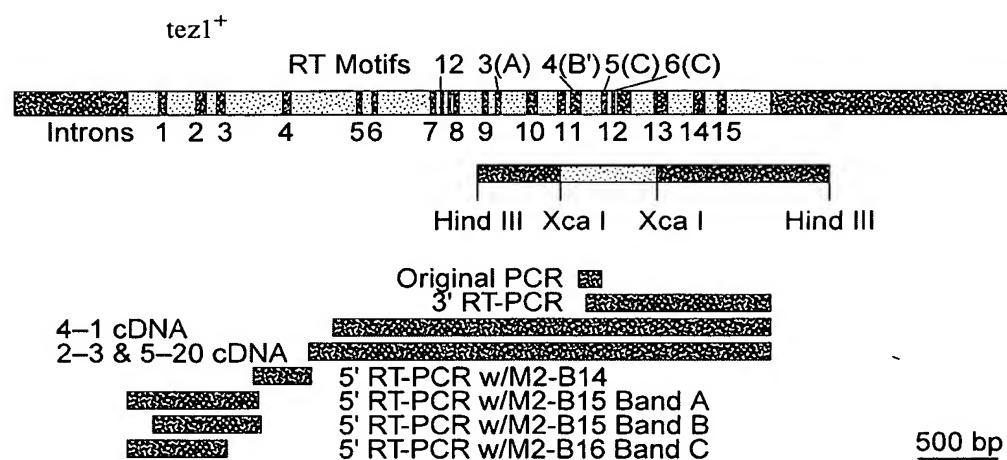
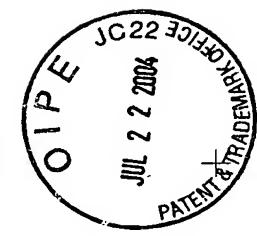


FIG. 33B



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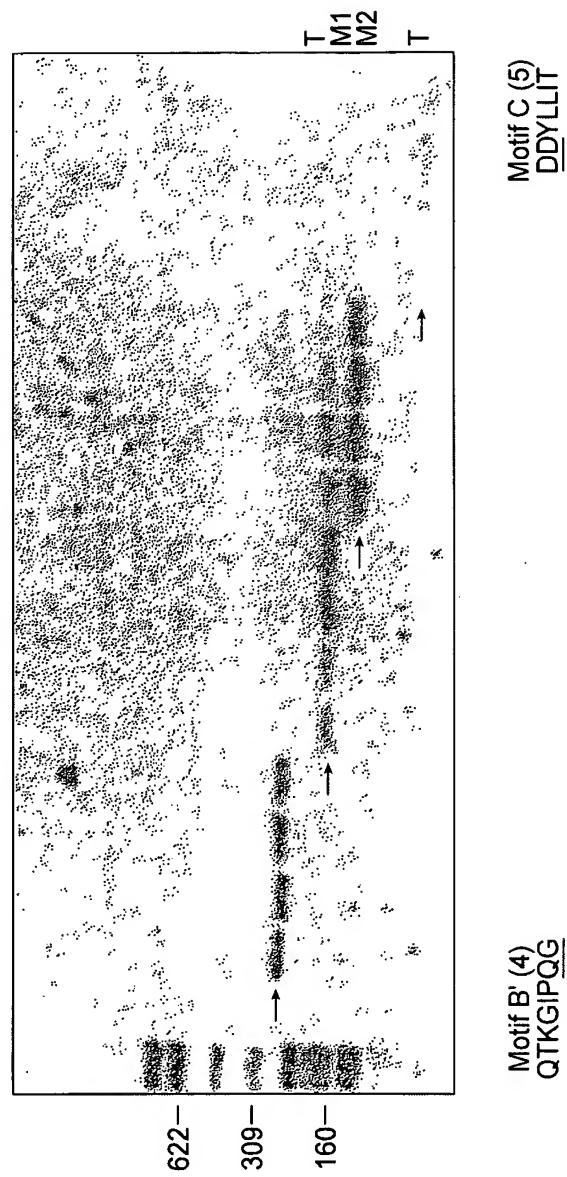


FIG. 35

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Ot	LCVSYIILSSFYANLEENALQFLRKESMDPEKPEPNLLMRILT
Ea_p123	KGIPQGLCVSSILSSFYATLEESSLGFLRDESMNPENPNVNLLMRILTDDYLLIT
Sp_M2	SILSSFLCHFYMEDLIDEYLSFTKKK-----GSVLLRVV
Sc_p103	DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLAADDLIIIS
	.* . * . * . *

Q K V G I P Q G
 caa aaa gtt ggt atc cct cag gg.....<---Actual Genomic Sequence.

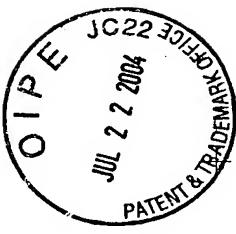
Poly 4
 t t t c
 t a g c c
 cag acc aaa gga att cca taa gg ---->

ag acc aaa gga att cca tca ggc TCA ATT CTG TCA TCT TTG TGT CAT TTC TAT ATG
 tc tgg ttt cct taa ggt agt ccg AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

K G I P S G S I L S S F L C H F Y M

F/G. 36A

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GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC CCT AGT CAC AAC AAT GCT
E D L I D E Y L S F T K K G S V L L R

GTA GTC gac gac tac ctc ctc atc acc
CAT CAG ctg ctg atg gag gag tag tgg

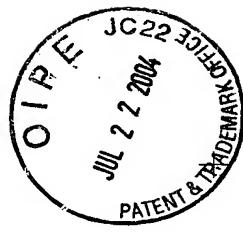
V V D D Y L L I T

<---- ctg ctg atg gag gag tag tgg
a a a a a a a a
t t t t t t
c c c c
Poly 1

.....gac gat ttc ctc ttt ata aca.....<---Actual Genomic Sequence
D D F L F I T

FIG. 36B

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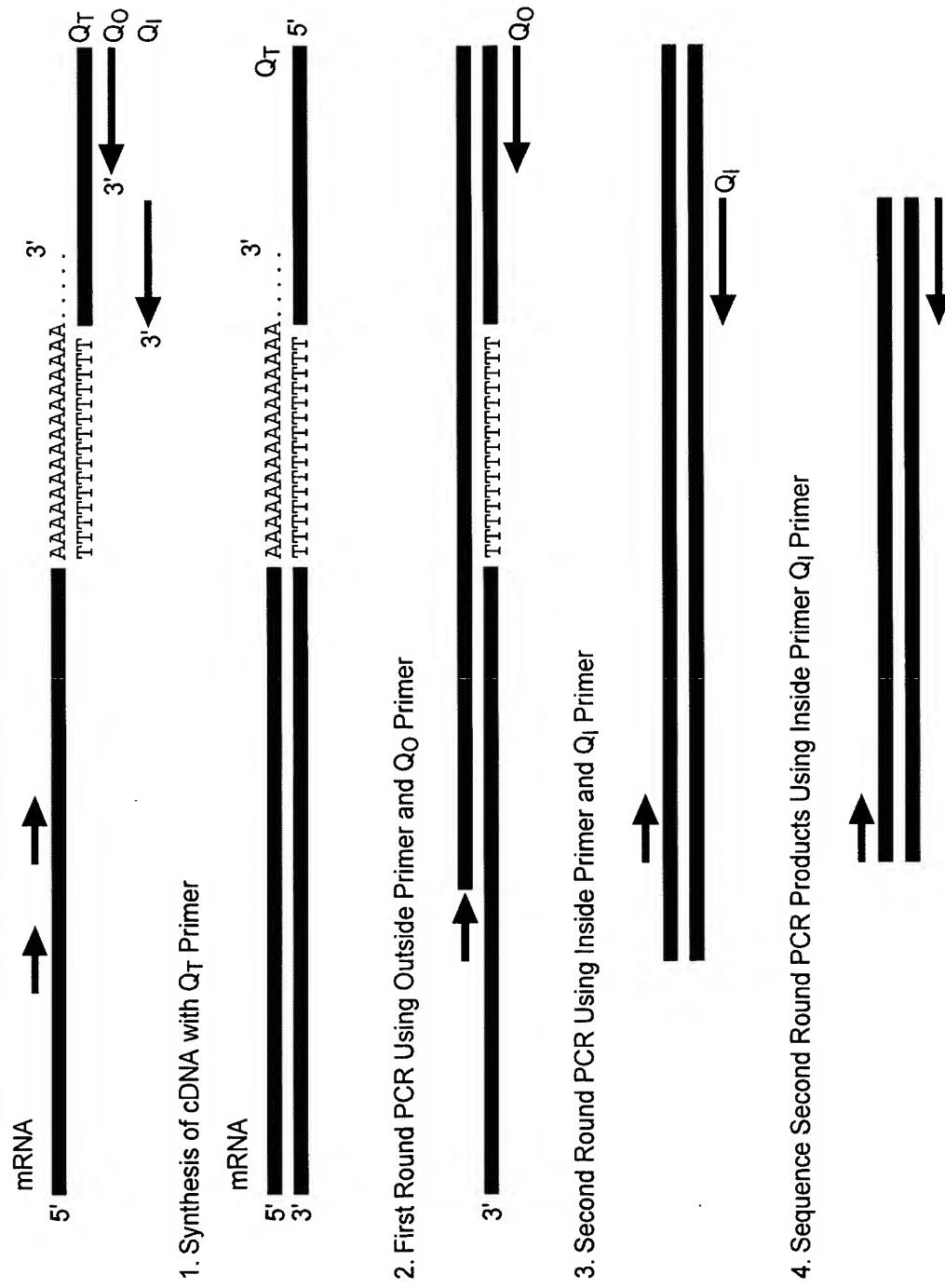
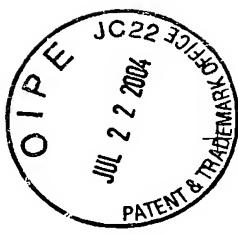


FIG. 37



A. Genomic Libraries

Size Selected Libraries from P. Nurse

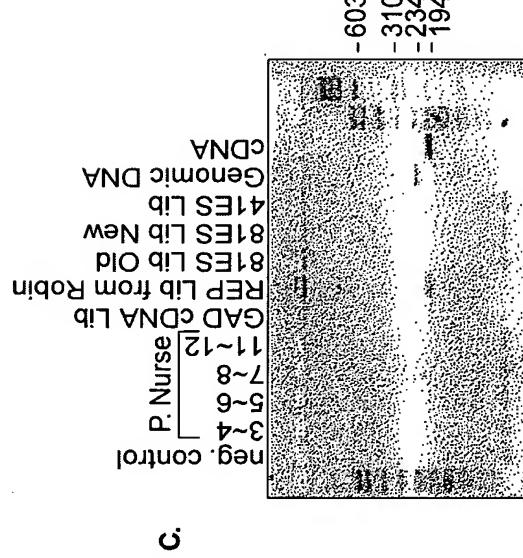
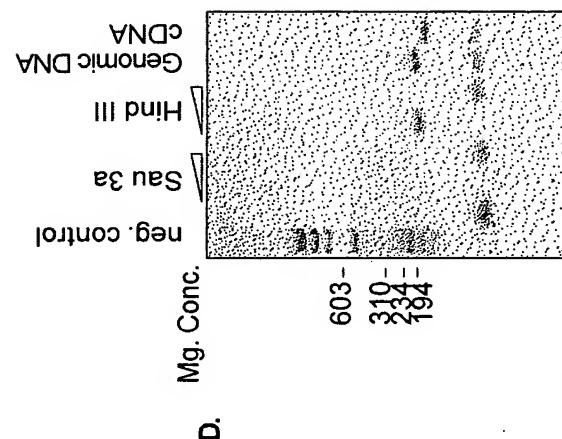
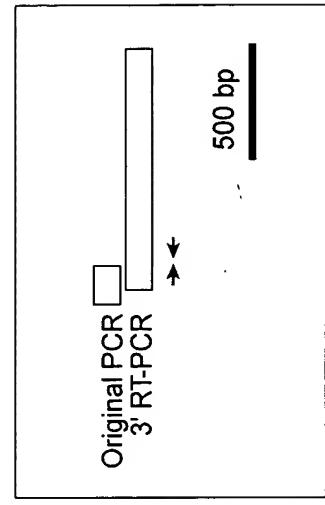
- 3~4 kb
- 5~7 kb
- 7~8 kb
- 11~12 kb

Libraries from J.A. Wise

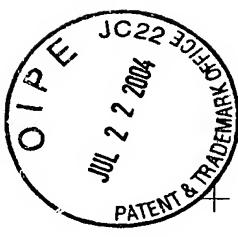
- Sau 3a Partial Digest
- Hind III Partial Digest

cDNA Libraries

- GAD (Gal Activation Domain) Library
- REP Library from R. Allshire
- REP81ES Library (old)
- REP81ES Library (new)
- REP41ES Library



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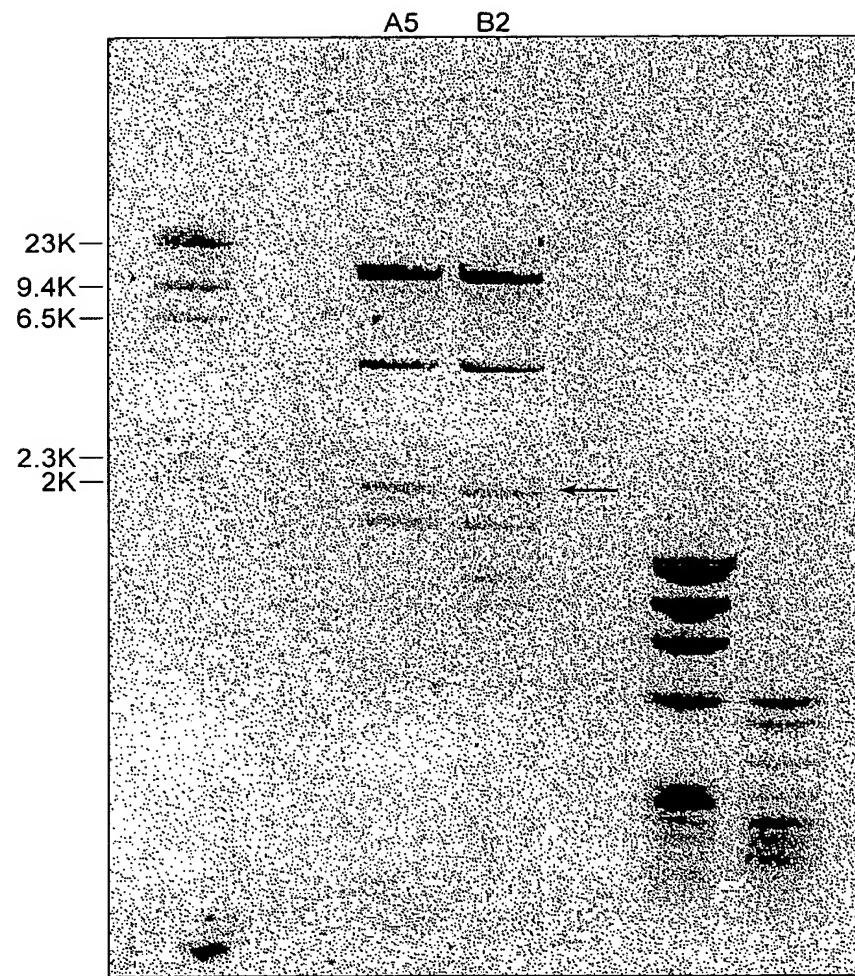
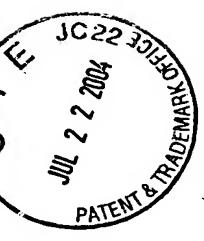


FIG. 39



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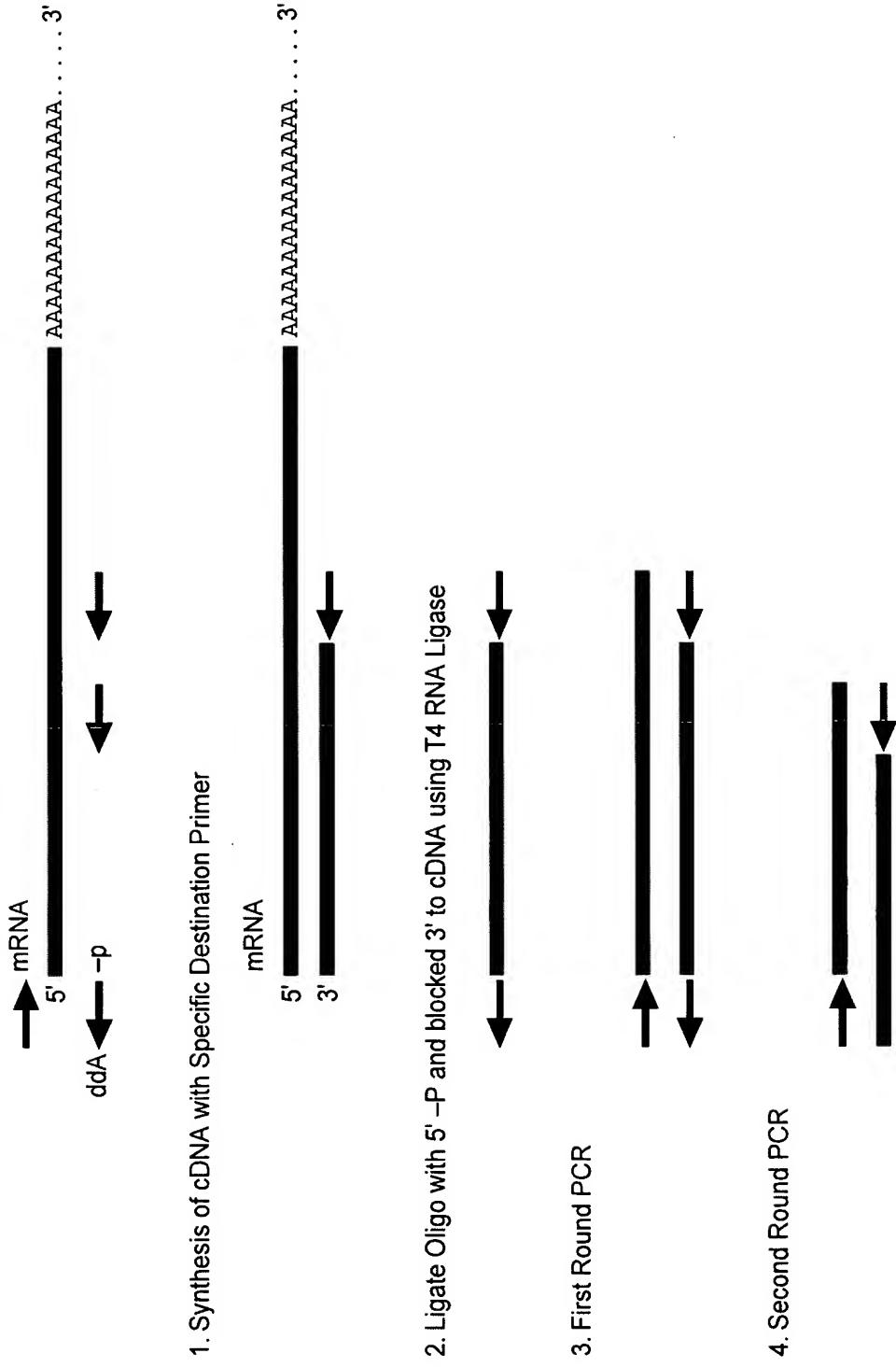
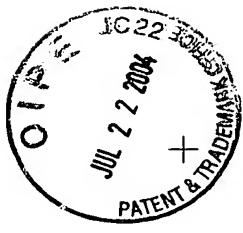


FIG. 40

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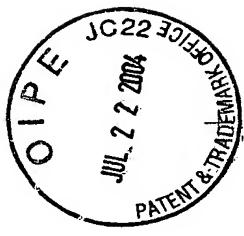


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S.p.	Tez1p	(429)	WLYNSFIIPILQSFYITESSDLRNRTVYFRKDIW	...	(35)	...	Motif 0
S.c.	Est2p	(366)	WLFRQLIPKIQIOTFFYCTEISSTVT - IVYFRHDTW	...	(35)	...	
E.a.	p123	(441)	WIFEDLVSLIRCFYYVTEQQSYSKTYYRKNIW	...	(35)	...	
		*	*** * *	*	*	*	
			Motif 1	Motif 2	K		
			P hh h	hR h	R		
S.p.	Tez1p	AVIRLLPKK--NTFRLITN-LRKRF	...	(61)	...		
S.c.	Est2p	SKMRLIPKKSNNNEFRRIIAIPCRGAD	...	(62)	...		
E.a.	p123	GKRLIPKK--TTFRPIMTFNKKIV	...	(61)	...		
		*	*** *	*	*	*	
			Motif 3 (A) AF				
			h hDh GY h				
S.p.	Tez1p	KKYFVRIDIKSCYDRIKQDLIMFRIVK	...	(89)	...		
S.c.	Est2p	ELYFMKEDVKSCYDSIPRMECMRILK	...	(75)	...		
E.a.	p123	KLFFATMDIEKCYDSVNREKLSTFLK	...	(107)	...		
		*	*** *	*	*	*	
			Motif 4 (B')				
			hPQG PP hh h				
S.p.	Tez1p	YLQKVGVIPQGSILSSFLCHFYMEDLIDEYLSF	...	(6)	...		
S.c.	Est2p	YIREDGFLFGQSSLSAPIVDLVYDDLLEFYSEF	...	(8)	...		
E.a.	p123	YKQTKGIPQGLCVSSILSSFYATLEESSLGF	...	(14)	...		
		*	*** *	*	*	*	
			Y Motif 5 (C)				
			h F DDhh				
S.p.	Tez1p	VLLRVDDFLFITVNKDAKKFLNLSLRGFFEKHNFSTSLLEKTVINFENS	...	(205)	...		Motif 6 (D)
S.c.	Est2p	LILKLAADDFLIIISTDQQQVINIKKLAMGGFQKYNAKANRDKILAVSSQS	...	(173)	...		
E.a.	p123	LILMRLTDDFLLITIQENNNAVLFIEKLINVSRENGFKPNMKKLQTSFPLS	...	(209)	...		
		*	*** *	*	*	*	

FIG. 41

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A.

Sp_Tip1p 1 - - - - - M T E H H T P K S R I L R F L E N Q Y Y L C T 24
 Sc_Est2p 1 - - - - - M E V D V D N Q A D N H G I H S A L K T C E E I K E A K T L Y S W 33
 Ea_p123 1

Sp_Tip1p 25 L N D Y V Q L V L R G S P A S S Y S N I C E R L R S D V Q T S F S 57
 Sc_Est2p 8 I Q D K L D I D L Q T N - S T Y K - - E N L K C G H F N G L D 35
 Ea_p123 34 I Q K V I R C R N Q S Q - S H Y K - - D L E D I K I F A Q T N 61

Sp_Tip1p 58 I F L H S T V V G F D S K P D E G V Q F S S P K C S Q S E L I A N 90
 Sc_Est2p 36 E I L T T C F A L P N S R - K I A L P C L P G D L S H K A V I D H 67
 Ea_p123 62 I V A T P R D Y N E E D F K V I A R K E V F S T G L M I E L I D K 94

Sp_Tip1p 91 Y V K Q M F D E S F E R R R - N L L M K G F S M N H E D F R A M H 122
 Sc_Est2p 68 C I Y L L T G E L Y N - N Y L T F G Y K I A R N E D - - - 93
 Ea_p123 95 C L V E L L S S S D V S D R Q K L Q C F G F Q L K G N Q - - - 122

Sp_Tip1p 123 V N G V Q N D L V S T F P N Y L I S I L E S K N W Q L L E I I G 155
 Sc_Est2p 94 - - V N N S L F C H S A N V N V T L L K G A A W K M F H S L V G 123
 Ea_p123 123 - - L A K T H L L T A L S T Q K Q Y F F Q D E W N Q V R A M I G 152

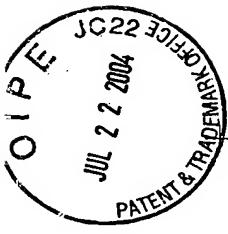
Sp_Tip1p 156 S D A M H Y L L S K G S I F E A L P N D N Y L Q I S G I P L F K N 188
 Sc_Est2p 124 T Y A F V D L L I N Y T V I Q F N - G Q F F T Q I V G N R C N E P 155
 Ea_p123 153 N E L F R H L Y T K Y L I F Q R T S E G T L V Q F C G N N V F D H 185

Sp_Tip1p 189 N V F E E T V S K K R K R T I E T S I T Q N - - - K S A R K E V S 218
 Sc_Est2p 156 H L P P K W V Q - R S S S S A T A A Q I - - - K Q L T E P V T 183
 Ea_p123 186 L K V N D K F D K - K Q K G G A A D M N E P R C C S T C K Y N V K 217

F/G. 42A



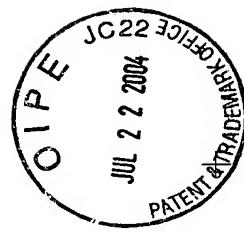
FIG. 42B



A.

Sp_Tip1p	426	EF[I]YWL[YNSFI[I]PIL[Q[SFFY[TE[SSDLRNRT[VY	458
Sc_Est2p	363	CF[I]SWL[F[Q[LI]PK[Q[TFY[CTE[ISST[V[- [VY	394
Ea_p123	438	KLLRWT[F[EDL[V[VSL[IR[CFYY[VTE[QQKSYSK[TYY	470
Sp_Tip1p	459	FRKD[I]WKL[LCRPF[I]TSMK[MEAF[EK[INENNVRMD	491
Sc_Est2p	395	FRHD[DTWNL[ITPF[I]VEY[FKTY[L[VENNYCRNHNNS	427
Ea_p123	471	YRK[N[I]WDV[IMKMSIA[DLKKE[TT[L[AEVQEKEYEEW	503
Sp_Tip1p	492	TQKTTL[P[PAY[I]RLL[P[KK[-NTFRL[ITNLR[KRFL	522
Sc_Est2p	428	YTLSNF[NH[SK[MR[ITPK[Q[NE[FR[IA[PCRGAD	460
Ea_p123	504	KKSLGFA[PGKL[RL[IPKK[-TTFRPIMTFNKKIV	534
Sp_Tip1p	523	IKMGSNK[KML[VST[NQTL[RP[VAS[IL[KHL[INE[-	552
Sc_Est2p	461	EEE[- FT[I]Y[K[ENHKN[AI]Q[PTQ[K[IE[Y[LRNKRPT	491
Ea_p123	535	NSD[- RK[T[TKL[TT[N[KL[SHL[ML[KTL[KNR[MF	564
Sp_Tip1p	553	ESSGI[P[FN[LEV[YMK[LL[TFK[KD[LL[KH[RMF[G[R[-KK	584
Sc_Est2p	492	SFTK[I]YSP[TQ[ADR[KEFK[QRL[LL[KFNNV[LP[EL	524
Ea_p123	565	KDPFGFA[V[FN[YDD[V[MK[YYEEF[V[CKWKQ[V[GQ[PKL	597
Sp_Tip1p	585	YF[V[R[DI[KSC[YDR[IKQDLM[F[R[IV[KKK[L[KDPE[F	616
Sc_Est2p	525	YF[MK[FD[Y[KSC[YDS[PR[MECM[R[IL[KDAL[KN[ENG[F	557
Ea_p123	598	FFATMD[IE[KCYDS[V[NREKL[ST[FL[KTTKL[SSDF	630
Sp_Tip1p	617	VIR[KYAT[I]HATSDRATKN[- - - - -	634
Sc_Est2p	558	FV[RSQYFFNTNTG[- - - - -	570
Ea_p123	631	WIMTAQ[ILKRKNN[I]VIDSKNFRKKEMKD[YFRQK	663

FIG. 42C



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FIG. 42D

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A.

Sp_Tip1p 850 **L****A****S****F****A****Q****V****F** **I** **D****I** **T****H****N****S****K****F****N****S****C****C****N** **I** **Y****R****L****G****Y****S****M****C****M****R** 882
 Sc_Est2p 773 **L****N****S****T****N****T****V****L****M****Q****I** **D****H****V****V****K****N****I** **S****E****C** - - - - - 793
 Ea_p123 895 **L****M****N****N****I** **T****H****Y****F****R****K****T** **I** **T****T****E****D****F****A****N****K****T****L****N****K****L****F** **I** **S****G****G****Y****K** 927

Sp_Tip1p 883 **A****Q****A****Y****L****K****R****M****K****D** **I** **F****I** **P****Q****R****M****F****I** **T****D****L****L****N****V****I** **G****R****K** **I** **W****K****K** 915
 Sc_Est2p 794 **-****-****-****-****Y****K****S****A****F****K****D****L****S****I** **N** - **V****T****Q****N****M****Q****F****H****S****F****L****Q****R** **I** **E****M** 821
 Ea_p123 928 **Y****M****Q****C****A****K****E****Y****K****D****H****F****K****K****N****L****A****M****S****S****M** **I** **D****L****E****V****S****K****I****I** **Y****S****V** 960

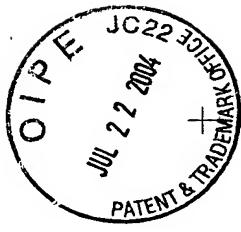
Sp_Tip1p 916 **L****A****E****I** **L****G****Y****T****S****R****R****F****L****S****S****A****E****V****K****W****L****F****C****L****G****M****R****D****G****L****K****P****S** 948
 Sc_Est2p 822 **T****V****S****G****C****P****I****T****K****C****D****P****L****I****E****Y****E****V****R****F****T****I** **L****N****G****F****L****E****S****L****S****S****N** 854
 Ea_p123 961 **T****R****A****F****F****K****Y****L****V****C****N** **I** **K****D****T****I** **F****G****E****E****H****Y****P****D****F****F****L****S****T****L****K****H****F** 993

Sp_Tip1p 949 **F****K****Y****H****P****C****F****E****Q****L****I** **Y****Q****F****Q****S****L****T****D****L****I****K****P****L****R****P****V****L****R****Q****V****L****F** 981
 Sc_Est2p 855 **T****S** - - - - - **-****-****-****-****-****K****F****K****D****N****I** **I****L****L****R****K****E****I****Q****H****L****Q****A****Y****I****Y** 877
 Ea_p123 994 **I****E****I****F****S** - - - **-****T****K****K****Y****I** **E****N****R****V****C****M****I****L****K****A****K****E****A****K****L****K****S****D****Q****C** 1023

Sp_Tip1p 982 **L****H****R****R****I****A****D** - - - - -
 Sc_Est2p 878 **-****I****Y****I****H****I****V****N****-**
 Ea_p123 1024 **Q****S****L****I****Q****Y****D****A**
 988
 884
 1031

F/G. 42E

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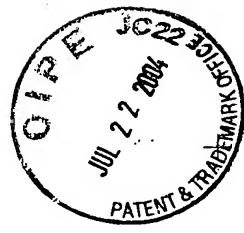
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B.

Sp_Tip1p	1	- - - - -	M T E H H T P K S R I L R F L E N Q Y V Y L C T	24
Sc_Est2p	1	- - - - -	- - - - - M K I L F E F	7
Ea_p123	1	M E V D V D N Q A D N H G I H S A L K T C E E I K E A K T L Y S W	33	
Sp_Tip1p	25	L N D Y V Q L V L R G S P A [S Y S N I C E R L R S D V Q T S F S	57	
Sc_Est2p	8	I Q D K L D I D L Q T N - - [S T Y K - - - E N L K C G H F N G L D	35	
Ea_p123	34	I Q K V I R C R N Q S Q - - [S H Y K - - - D L E D I K I F A Q T N	61	
Sp_Tip1p	58	I F L H S T V V G F D S K P D E G V Q F S S P K C S Q S E L [I A N	90	
Sc_Est2p	36	E I L T C F A L P N S R - K I A L P C L P G D L S H K A V I D H	67	
Ea_p123	62	I V A T P R D Y N E E D F K V I A R K E V F S T G L M I E L I D K	94	
Sp_Tip1p	91	V V K Q M F D E S F E R R R - N L L M K G F S M N H E D F R A M H	122	
Sc_Est2p	68	C I Y L L T G E L Y N - - N V L T F G Y K I A R N E D - - -	93	
Ea_p123	95	C L V E L L S S S D V S D R Q K L Q C F G F Q L K G N Q - - -	122	
Sp_Tip1p	123	V N G V Q N D L V S T F P N Y L I S I L E S K N [W Q L L E I I G	155	
Sc_Est2p	94	- - V N N S L F C H S A N V N V T L L K G A A W K M F H S L V G	123	
Ea_p123	123	- - L A K T H L L T A L S T Q K Q Y F F Q D E W N Q V R A M I G	152	
Sp_Tip1p	156	S D A M H Y L L S K G S I F E A L P N D N Y L Q I S G I P L F K N	188	
Sc_Est2p	124	T Y A F V D L L I N Y T V I Q F N - G Q F F T Q I V G N R C N E P	155	
Ea_p123	153	N E L F R H L Y T K Y L I F Q R T S E G T L V Q F C G N N V F D H	185	
Sp_Tip1p	189	N V F E E T V S K K R K R T I E T S I T Q N - - - K S A R K E V S	218	
Sc_Est2p	156	H L P P K W V Q - - R S S S S A T A A Q I - - - K Q L T E P V T	183	
Ea_p123	186	L K V N D K F D K - K Q K G G A A D M N E P R C C S T C K Y N V K	217	

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B.

Sp_Tip1p	219	WN S I S I S R F S I F Y R S S Y K K F K Q D L Y F N L H S I C D	251	
Sc_Est2p	184	N - - - - -	K Q F L H K L N I N S S F F P	200
Ea_p123	218	N E K - - - - -	D H F L N N I N V P N W N N M K S R T R I F Y C T H F N	248
Sp_Tip1p	252	R N T V H M W L Q W I F P R Q F G L I N A F Q V K Q L H K V I P L	284	
Sc_Est2p	201	- - - - - Y S K I L P S S S - - - S I K K L T D L R E A I F P	223	
Ea_p123	249	R - - - - - N N Q F F K K H E F V S N K N N I S A M D R A Q T I	275	
Sp_Tip1p	285	V S - - - Q S T V V P K R L L K V Y P L I E Q T A K R L H R I S	313	
Sc_Est2p	224	T N - - - L V K I P Q R L K V R I N L T L Q K L L K R H K R L N	252	
Ea_p123	276	F T N I F R F N R I R K K L K D K V I E K I A Y M L E K V K D F N	308	
Sp_Tip1p	314	L S K V Y N H Y C P Y I D - T H D D E K I L S Y S L K P N Q - - -	342	
Sc_Est2p	253	Y V S I L N S I C P P L E G T V D D L S H L S R Q S P K E R - - -	282	
Ea_p123	309	F N Y Y L T K S C P L P E N W R E R K Q K I E N L I N K T R E E K	341	
Sp_Tip1p	343	- -	359	
Sc_Est2p	283	- -	299	
Ea_p123	342	S K Y Y E E L F S Y T T D N K C Y T Q F I N E F F Y N I L P K D F	374	
Sp_Tip1p	360	W G N Q R I F E I I L K D L E T F L K L L S R Y E S F S L H Y [M S	392	
Sc_Est2p	300	F G S K K N K G K I I K N L N L L S L P L N G Y L P F D S L L K	332	
Ea_p123	375	L T G - R N R K N F Q K K V K K V Y V E L L N K H E L I H K N L L E	406	
Sp_Tip1p	393	N I K I S E I E W L V L G K R S N A K M C L S D F E K R K Q I F A	425	
Sc_Est2p	333	K L R L K D F R W L F I S - - D I W F T K H N F E N L N Q L A I	362	
Ea_p123	407	K I N T R E I S W M Q V E T S - A K H F Y Y F D H E N - I Y V L W	437	

F/G. 42G

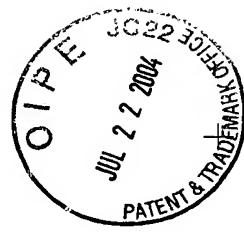
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B.

Sp_Tip1p	426	EE I YWL YNSF I IPI L Q SFF Y I TE S S D L R N R T V Y	458
Sc_Est2p	363	CF I SWL F R Q L I P K I I Q T F F Y C T E I S S T V T - I V Y	394
Ea_p123	438	K L L R W I F E D L V V S L I R C F F Y V T E Q Q K S Y S K T Y Y	470
Sp_Tip1p	459	FR K D I W K L L C R P F I T S M K M E A F E K I N E N N V R M D	491
Sc_Est2p	395	FR H D T W N K L I T P F I V E Y F K T Y L V E N N V C R N H N S	427
Ea_p123	471	Y R K N I W D V I M K M S I A D L K K E T L A E V Q E K E E W	503
Sp_Tip1p	492	T Q K T T L P P A V I R L L P K K - - N T F R L I T N L R K R F L	522
Sc_Est2p	428	Y T L S N F N H S K M R I I P K K S N N E F R I I A I P C R G A D	460
Ea_p123	504	K K S L G F A P G K L R L I P K K - - T T F R P I M T F N K K I V	534
Sp_Tip1p	523	I K M G S N K K M L V S T N Q T L R P V A S I L K H L I N E - -	552
Sc_Est2p	461	EE E - - F T I Y K E N H K N A I Q P T Q K I L E Y L R N K R P T	491
Ea_p123	535	N S D - - R K T T K L T T N T K L L N S H L M L K T L K N R - M F	564
Sp_Tip1p	553	E S S G I P F N L E V Y M K L L T F K K D L L K H R M F G R - K K	584
Sc_Est2p	492	S F T K I Y S P T Q I A D R I K E F K Q R L L K K F N N V L P E L	524
Ea_p123	565	K D P F G F A V F N Y D D V M K K Y E E F V C K K W K Q V G Q P K L	597
Sp_Tip1p	585	Y F V R I D I K S C Y D R I K Q D L M F R I V K K K L K D P E - F	616
Sc_Est2p	525	Y F M K F D V K S C Y D S I P R M E C M R I L K D A L K N E N G F	557
Ea_p123	598	F F A T M D I E K C Y D S V N R E K L S T F L K T T K L L S S D F	630
Sp_Tip1p	617	V I R K Y A T I H A T S D R A T K N - - - - -	634
Sc_Est2p	558	F V R S Q Y F F N T N T G - - - - -	570
Ea_p123	631	W I M T A Q I L K R K N N I V I D S K N F R K K E M K D Y F R Q K	663

F/G. 42H



B.

Sp_Tip1p	635	F V S E A F S Y F D M V P F E K V V Q L L S - - M K T S D T L F V	665
Sc_Est2p	571	- - - - - V L K L F N V V N A S R - - V P K P Y E L Y -	591
Ea_p123	664	F Q K I A L E G G Q Y P T L F S V L E N E Q N D L N A K K T L I V	696
Sp_Tip1p	666	D F V D Y W T K S S S E I F K M L K E H L S G H I V K I G N S Q Y	698
Sc_Est2p	592	D N V R T V H L S N Q D V I N V V E M E I F K T A L W W E D K C Y	624
Ea_p123	697	E A K Q R N Y F K K D N N L L Q P V I N I C Q Y N Y I N F N G K F Y	729
Sp_Tip1p	699	L Q K V G I P Q G S I L S S F L C H F Y M E D L I D E Y L S F T K	731
Sc_Est2p	625	I R E D G L F Q G S S L S A P I V D L V Y D D L L E F Y S E F K A	657
Ea_p123	730	K Q T K G I P Q G L C V S S I L S S F Y Y A T L E E S S L G E L R	762
Sp_Tip1p	732	K K G - - - - - S V L L R V V D D F L F I T V N K K D A K K	756
Sc_Est2p	658	S P S Q D - - - - - T L I L K L A D D F L I I S T D Q Q Q V I N	684
Ea_p123	763	D E S M N P E N P N V N L L M R L T D D Y L L I T T Q E N N A V L	795
Sp_Tip1p	757	F L N L S L R G F E K H N F S T S L E K T V I N F E N S N G - - -	786
Sc_Est2p	685	I K K L A M G G F Q K Y N A K A N R D K I L A V S S Q S D - - -	713
Ea_p123	796	F I E K L I N V S R E N G F K F N M K K L Q T S F P L S P S K F A	828
Sp_Tip1p	787	- - - I I N N T F F N E S K K R M P F F G F S V N M R S L D T L L	816
Sc_Est2p	714	- - - D D T V I Q F C A - - M H I F V K E L E V W K H S S T M	739
Ea_p123	829	K Y G M D S V E E Q N I V Q D Y C D W I G I S I D M K T L A L M P	861
Sp_Tip1p	817	A C P K I D E A L F N S T S V E L T K H M G K S F F Y K I L R S S	849
Sc_Est2p	740	N N F H I R S K S S K G I F R S L I A L F N T R I S Y K T I D T N	772
Ea_p123	862	N I N L R I E G I L C T L N L N M Q T K K A S M W L K K L K S F	894

FIG. 42/

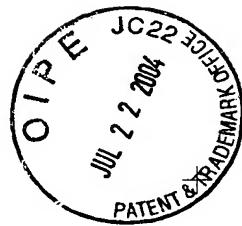


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B.	Sp_Tip1p	850	[LASFAQVFI DITHNSKFNSCCN IYRLGYSMCMR	882
	Sc_Est2p	773	[LNSTNTVLMQIDHVVKN ISEC - - -	793
	Ea_p123	895	[LMNNITHYFRKT ITTEDFANKTLNKLFI SGGYK	927
	Sp_Tip1p	883	AQAYLKRMDIFIPQRMFI TDLLNVIGRKIWKK	915
	Sc_Est2p	794	- - - YKSAFKDLSIN - VTQNMQFHSFLQR - - -	821
	Ea_p123	928	YMQCAKEYKDHFKKNLAMSSMIDLEVS KI YSV	960
	Sp_Tip1p	916	LAEILGYTSRRFLSSAEVKWLFCLGMRDGLKPS	948
	Sc_Est2p	822	TVSGCPITKCDPLIEYEVRFTILNGFLESLSNN	854
	Ea_p123	961	TRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHF	993
	Sp_Tip1p	949	FKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLF	981
	Sc_Est2p	855	TS - - - - KFKDNILLRKEIQHLQAYIY	877
	Ea_p123	994	IEIFS - - - TKKYIFNRVCMLKAKEAKLKSDQC	1023
	Sp_Tip1p	982	LHRRRIAD -	988
	Sc_Est2p	878	- - - YIHIVN -	884
	Ea_p123	1024	QSLIQYDA	1031

FIG. 42J

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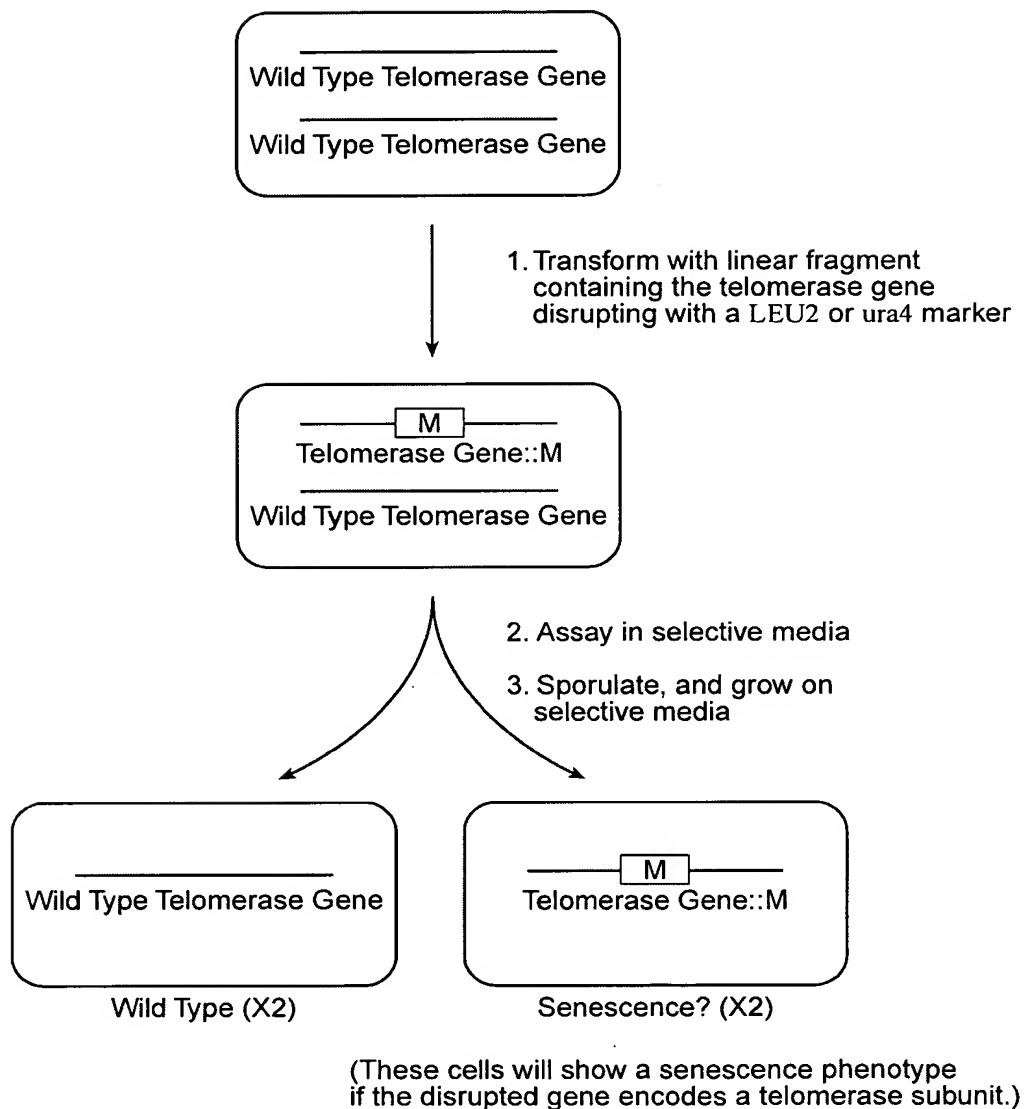


FIG. 43

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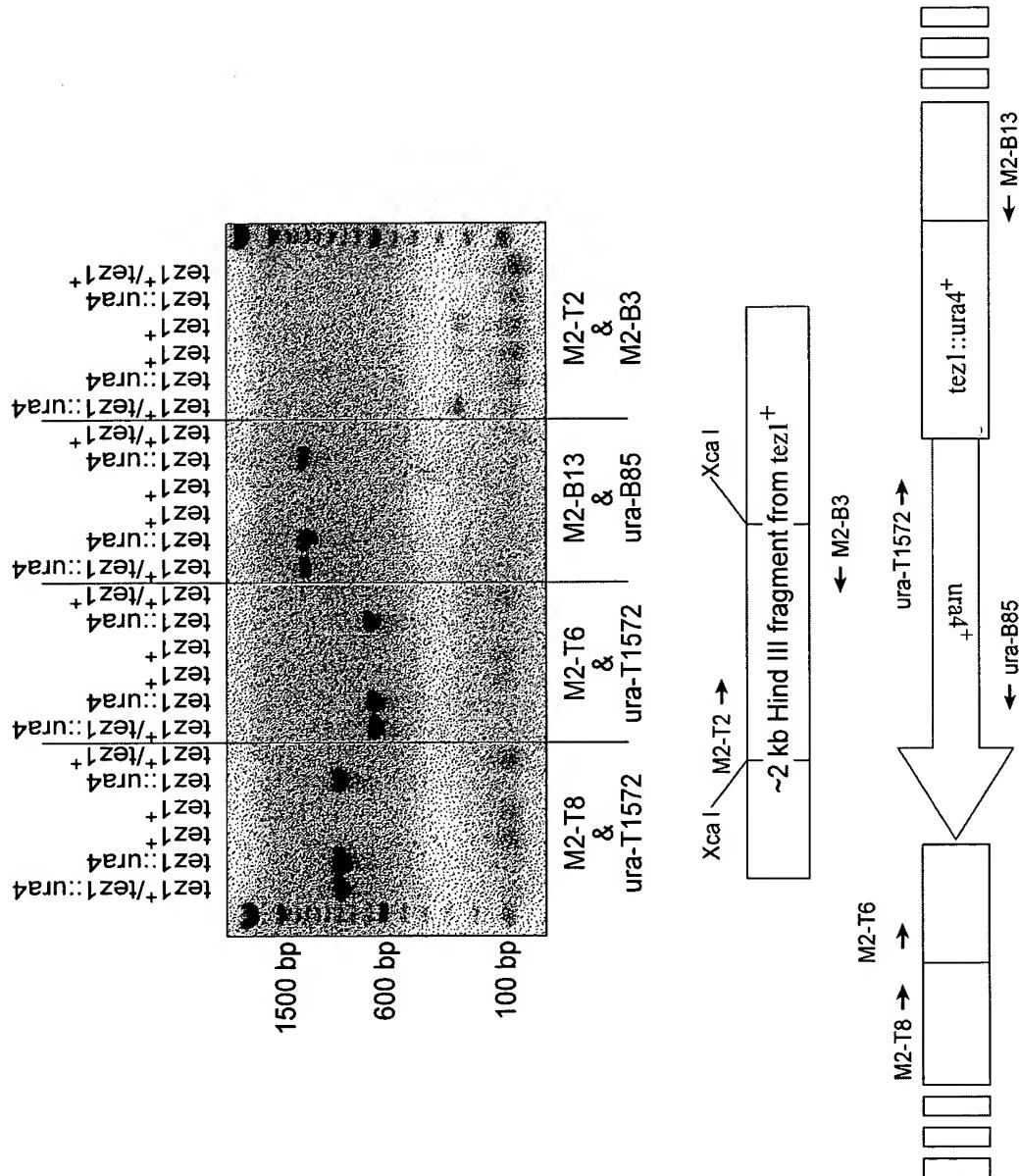
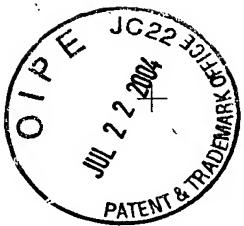
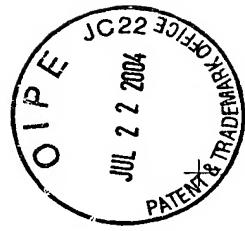


FIG. 44



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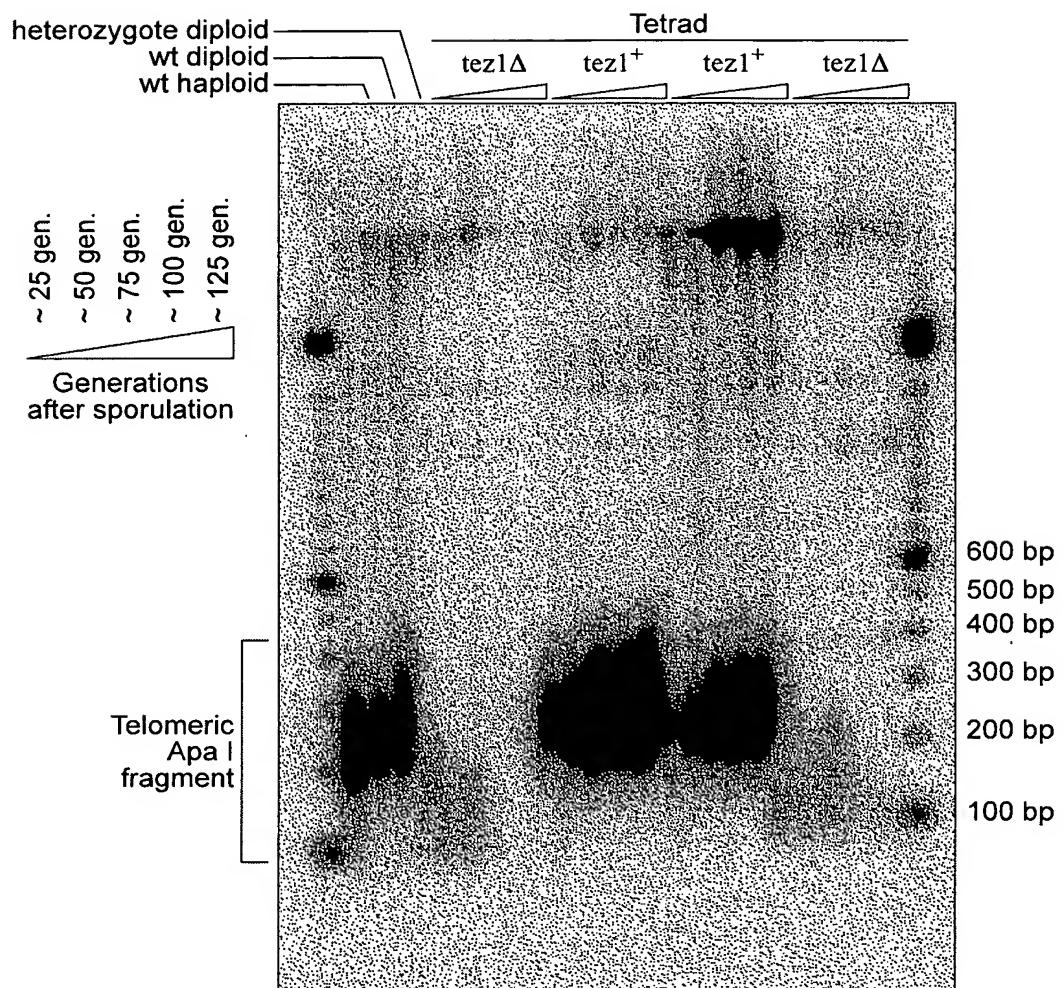
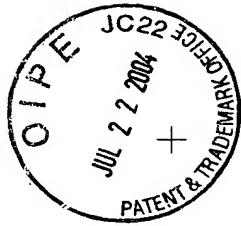
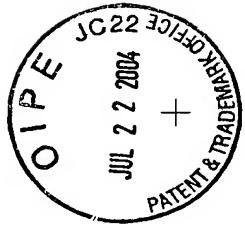


FIG. 45



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FIG. 46A



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1470	GAT	CTC	GTT	TCT	ACT	TTT	CCT	AAT	TAC	CCT	ATA	TCT	ATA	CTT	GAG	TCA	AAA	AAT	TGG	CAA	1529	
129	D	L	V	S	T	F	P	N	Y	L	I	S	I	L	E	S	K	N	W	Q	148	
149	L	L	L	E	I												I	G	155			
1530	CRT	TTG	TTA	GAA	AT	gttaataccgggttaaggatgtggcactttgaacaagactgacaatag	T	ATC	GCC	1601												
156	S	D	A	M	H	Y	L	L	S	K	G	S	I	F	E	A	L	P	N	D	175	
1602	AGT	GAT	GCC	ATG	CAT	TAC	TTA	TTA	TCC	AAA	GGA	AGT	ATT	TTT	GAG	GCT	CTT	CCA	AAT	GAC	1661	
156	S	D	A	M	H	Y	L	L	S	K	G	S	I	F	E	A	L	P	N	D	175	
1662	AAT	TAC	CTT	CAG	ATT	TCT	GGC	ATA	CCA	CTT	TTT	AAA	AAT	AAT	GTG	TTT	GAG	GAA	ACT	GTG	1721	
176	N	Y	L	Q	I	S	G	I	P	L	F	K	N	N	V	F	E	E	T	V	195	
1722	TCA	AAA	AAA	AGA	AAG	CGA	ACC	ATT	GAA	ACA	TCC	ATT	ACT	CAA	AAT	AAA	AGC	GCC	CGC	AAA	1781	
196	S	K	K	R	K	R	T	I	E	T	S	I	T	Q	N	K	S	A	R	K	215	
1782	GAA	GTT	TCC	TGG	ATT	AGC	ATT	TCA	ATT	AGT	AGG	TTT	AGC	ATT	TTT	TAC	AGG	TCA	TCC	TAT	1841	
216	E	V	S	W	N	S	I	S	R	F	S	I	F	S	I	F	Y	R	S	S	Y	235
1842	AAG	AAG	TTT	AAG	CAA	G	gttaactaataactgttatccttcataactaatttttag	AT	CTA	TAT	TTT	AAC	1907									
236	K	F	K	Q	D											L	Y	F	N		245	
1908	TTA	CAC	TCT	ATT	TGT	GAT	CGG	AAC	ACA	GTA	CAC	ATG	TGG	CTT	CAA	TGG	ATT	TTT	CCA	AGG	1967	
246	L	H	S	I	C	D	R	N	T	V	H	M	W	L	Q	W	I	F	P	R	265	
1968	CMA	TTT	GGA	CCT	ATA	AAC	GCA	TTT	CAA	GTG	AAG	CAA	TTG	CAC	AAA	GTG	ATT	CCA	CTTG	GTA	2027	
266	Q	F	G	L	I	N	A	F	Q	V	K	Q	L	H	K	V	I	P	L	V	285	
2028	TCA	CAG	AGT	ACA	GTT	GTG	CCC	AAA	CGT	CTC	CTA	AAG	GTA	TAC	CCT	CCT	TTA	ATT	GAA	CAA	ACA	2087
286	S	Q	S	T	V	V	P	K	R	L	L	K	V	Y	P	L	I	E	Q	T	305	
2088	GCA	AAG	CGA	CTC	CAT	CGT	ATT	TCT	CTA	TCA	AAA	GTT	TAC	AAC	CAT	TAT	TGG	CCA	TAT	ATT	2147	
306	A	K	R	L	H	R	I	S	L	S	K	V	Y	N	H	Y	C	P	Y	I	325	
2148	GAC	ACC	CAC	GAT	GAA	AAA	ATC	CCT	AGT	TAT	TCC	TTA	AAG	CCG	AAC	CAG	GTG	TTT	GCG	2207		
326	D	T	H	D	E	K	I	L	S	Y	S	L	K	P	N	Q	V	F	A	345		
2208	TTT	CTT	CGA	TCC	ATT	CTT	GTT	CGA	GTG	TTT	CCT	AAA	TTA	ATC	TGG	GGT	AAC	CAA	AGG	ATA	2267	
346	F	L	R	S	I	L	V	R	V	F	P	K	L	I	W	G	N	Q	R	I	365	

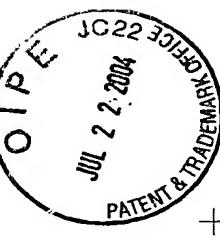
F/G. 46B



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FIG. 46C

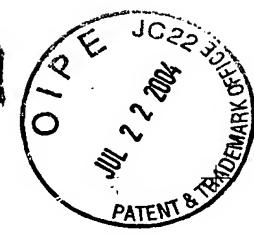
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EIG 46D

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3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT 3960
 799 R M P F G F S V N M R S L D T L A C 818
 3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG 4020
 819 P K I D E A L F N S T S V E L T K H M G 838
 4021 AAA TCT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaaataatcgacaaataatcg A TCG 4089
 839 K S F F Y K I L R S 848
 4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT 4149
 849 S L A S F A Q V F I D I T H N S K F N S 868
 4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA 4209
 869 C C N I Y R L G Y S M C M R A Q A Y L K 888
 4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G 9ttagtacttttaactaga 4274
 889 R M K D I F I P Q R M F I T D 903
 4275 aaagtattaaataacccttag AT CTT TTG ATT GTT ATT GGA AGA AAA ATT TTG AAA AAG TTG GCC 4339
 904 L L N V I G R K I W K K L A 917
 4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401
 918 E I L G Y T S R R F L S S A E V K W 935
 4402 ggctcggacttcggcaatttgcacatcg G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA 4468
 936 L F C L G M R D G L K 946
 4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT 4528
 947 P S F K Y H P C F E Q L I Y Q F Q S L T 966
 4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA 4588
 967 D L I K P L R P V L R Q V L F L H R R I 986
 4589 GCT GAT TAA tgtcattttcaatttatacatcccttattactgggtcttaaaacaataattactaagtata 4665
 987 A D * 989

FIG. 46E

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FIG. 46F



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1
GCCAAGTTCCCTGCACTGGCTG met ser val tyr val val glu leu leu
ATG AGT GTG TAC GTC GTC GAG CTG CTC

10 20
arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG

30
leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT

40 50
gly ile arg gln his leu lys arg val gln leu arg glu leu ser
GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG

60
glu ala glu val arg gln his arg glu ala arg pro ala leu leu
GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG

70 80
thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG

90
ile val asn met asp tyr val val gly ala arg thr phe arg arg
ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA

100 110
glu lys ala glu arg leu thr ser arg val lys ala leu phe
GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC

120
ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC

130 140
ala ser val leu gly leu asp asp ile his arg ala trp arg thr
GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC

150
phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCT GAG CTG TAC

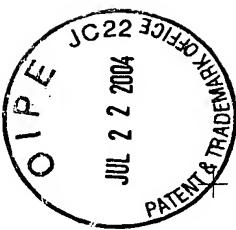
160 170
phe val lys val asp val thr gly ala tyr asp thr ile pro gln
TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG

180
asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC AAA CCC CAG AAC

190 200
thr tyr cys val arg arg tyr ala val val gln lys ala ala met
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG

FIG. 47A

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210
gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys
GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC
220 230
gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser
CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC
240
leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG
250 260
arg asp gly leu leu leu arg leu val asp asp phe leu leu val
CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG
270
thr pro his leu thr his ala lys thr phe leu arg thr leu val
ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC
280 290
arg gly val pro glu tyr gly cys val val asn leu arg lys thr
CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA
300
val val asn phe pro val glu asp glu ala leu gly gly thr ala
GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT
310 320
phe val gln met pro ala his gly leu phe pro trp cys gly leu
TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG
330
leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser
CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC
340 350
tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly
TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC
360
phe lys ala gly arg asn met arg arg lys leu phe gly val leu
TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG
370 380
arg leu lys cys his ser leu phe leu asp leu gln val asn ser
CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC
390
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG
400 410
ala tyr arg phe his ala cys val leu gln leu pro phe his gln
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

FIG. 47B

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420
gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430 440
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

450
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460 470
arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

480
thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490 500
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

510
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

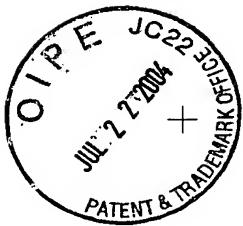
520 530
his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

540
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550 560
arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564
OP
TGA GTGAGTGTGTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC
CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTCACTTCCCCAC
AGGCTGGCGTTGGTCCACCCCAAGGGCCAGCTTTCCTCACCAAGGAGCCGGCTTCCACT
CCCCACATAGGAATAGTCCATCCCCAGATTGCCATTGTTCACCCCTGCCCTGCCCTCC
TTTGCCTTCCACCCCAACCATTAGGTGGAGACCTGAGAAGGACCTGGAGCTTGG
AATTGGAGTGACCAAGGTGTGCCCTGTACACAGGGAGGACCTGCACCTGGATGGGG
GTCCCTGTGGGTCAAATTGGGGGAGGTGCTGTGGAGTAAATACTGAATATATGAGTT
TTTCAGTTTGGAAAAAAAAAAAAAAAAAAAAAA

FIG. 47C

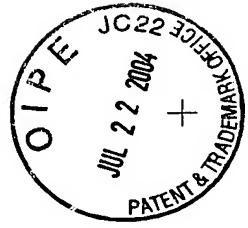


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Motif -1
Ep p123	LVVSLIRCFYYVTEQQKSYSKT...	FIIPILQSFFYITESSDLRNRT...	LIPKIIQTFFYCTEISSTVTIV...	YVVELLRSFFYVTETTFQKNRL...	
Sp Tez1				FFY TE	
Sc Est2					
Hs TCP1					
consensus					
K					
Motif 0	p hh	hR	h	R	
Ep p123	...KSLGFAPGKLRLIPKKT--TFRPIMTFNKKIV...	...QKTTLPPAVIRLLPKKN--TFRLITNLRKRLF...	...TLSNFNHSKMRIIPKKSNNFRIIAIPCRGAD...	...ARPALLTSRRLFIPKPD--GLRPIVNMDYVVG...	
Sp Tez1					
Sc Est2					
Hs TCP1					
consensus	R PK		R I		
AF					
Motif A	h hDh	GY	h		
Ep p123	...PKLFFATMDIEKCYDSVNREKLSTFLK...	...RKKYFVRIDIJKSCYDRIKQDLMFRIVK...	...PELYFMKFDVKSCYDSIPRMECMRILK...	...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...	
Sp Tez1					
Sc Est2					
Hs TCP1					
consensus	F D		YD		
hPQG pS hh					
Motif B	
Ep p123	...NGKFYKQTKGIPQGLCVSSILSSFYA...	...GNSQYLQKVGIPOQGSILSSFLCHFYME...	...EDKCYIREDGLFQGSSLSAPIVDLVYD...	...RATSYVQCQGIPQGSILSTLLCSLCYG...	
Sp Tez1					
Sc Est2					
Hs TCP1					
consensus	G QG		S		
Y					
Motif C	h F DD	hhh			
Ep p123	...PNVNLLMRLTDYLLITTQENN...	...KKGSVLLRVVDDFLFITVNKKD...	...SQDTLILKLADDFLIISTDQQQ...	...RRDGLLLRLVDDFLLVTPHLTH...	
Sp Tez1					
Sc Est2					
Hs TCP1					
consensus	DD L				
Gh h cK					
Motif D	
Ep p123	NVSRENGFKFNMKKL...	LNLSLRGFEKHNFST...	KKLAMGGFQKYNAKA...	LRTLVRGVPEYGCVV...	
Sp Tez1					
Sc Est2					
Hs TCP1					
consensus	G				

FIG. 48

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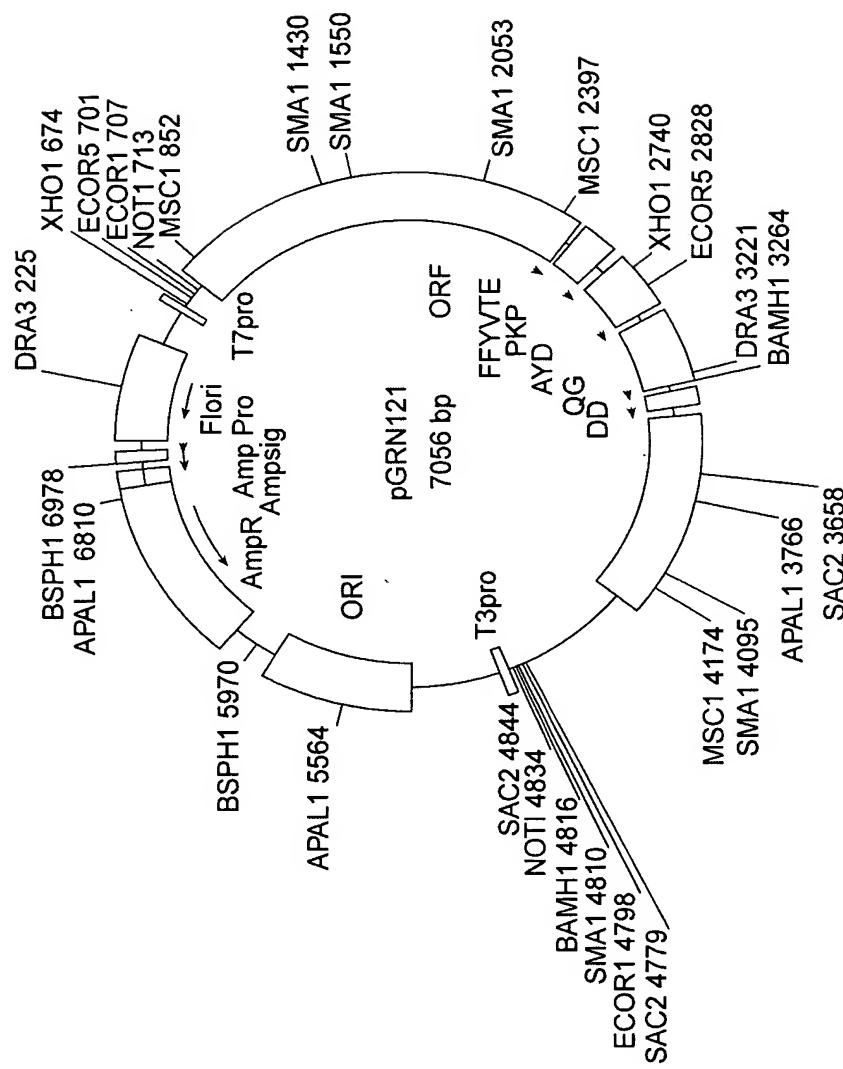
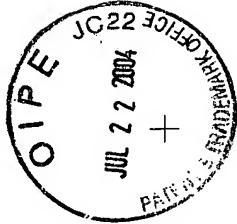


FIG. 49

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1	GCAGCGCTGC	GTCCTGCTGC	GCACGTGGGA	AGCCCTGGCC	CCGGCCACCC
51	CCCGGATGCC	GCGCGCTCCC	CGCTGCCGAG	CCGTGCGCTC	CCTGCTGCGC
101	AGCCACTACC	GCGAGGGTGT	GGCGCTGGCC	ACGTTCGTGC	GGCGCCTGGG
151	GCCCCAGGGC	TGGCGGCTGG	TGCAGCGCGG	GGACCCGGCG	GCTTCCGCG
201	CGNTGGTGGC	CCANTGCNTG	GTGTGCGTGC	CCTGGGANGN	ANGGCNGCCC
251	CCCGCCGCC	CCTCCTTCCG	CCAGGGTGTCC	TGCTCTGAANG	ANCTGGTGGC
301	CCGAGTGCTG	CANANGCTGT	GCGANCGCGG	CGCGAANAAAC	GTGCTGGCCT
351	TCGGCTTCGC	GCTGCTGGAC	GGGGCCCCCG	GGGGCCCCCC	CGAGGCCCTTC
401	ACCACCAAGCG	TGCGCAGCTA	CCTGCCAAC	ACGGTGACCG	ACGCAC TGCG
451	GGGGAGCGGG	GCGTGGGGGC	TGCTGCTGCG	CCCGCTGGG	GACGACGTGC
501	TGGTCACCT	GCTGGCACGC	TGCGCGNTNT	TTGTGCTGGT	GGNTCCCAGC
551	TGCGCCTACC	ANGTGTGCGG	GGCGCCGCTG	TACCAAGCTCG	CCGCTGCNAC
601	TCAGGCCCCG	CCCCCGCCAC	ACGCTANTGG	ACCCGAANGC	GTCTGGGATC
651	CAACGGGCCT	GGAACCATAG	CGTCAGGGAG	GCGGGGGTCC	CCCTGGGCTG
701	CCAGCCCCGG	GTGCGAGGAG	GCGCGGGGGC	AGTGCCAGCC	GAAGTCTGCC
751	GTTGCCAAG	AGGCCAGGC	GTGGCGCTGC	CCCTGAGCCG	GAGCGGACGC
801	CCGTTGGGCA	GGGGTCTCTGG	GGCCACCCGG	GCAGGACGCC	TGGACCGAGT
851	GACCGTGGTT	TCTGTGTGGT	GTCACCTGCC	AGACCCGCCG	AAGAACCCAC
901	CTCTTGGAG	GGTGCCTCT	CTGGCACCGC	CCACTCCCAC	CCATCCGTGG
951	GCCGCCAGCA	CCACGCCGGC	CCCCCATCCA	CATCGCGGCC	ACCACGTCC
1001	GGGACACGCC	TTGTCCCCCG	GTGTACGCCG	AGACCAAGCA	CTTCCTCTAC
1051	TCCTCAGGCG	ACAAGNACAC	TGCGNCCCTC	CTTCCTACTC	AATATATCTG
1101	AGGCCAGGCC	TGACTGGCGT	TCGGGAGGTT	CGTGGAGACA	NTCTTCTGG
1151	TTCCAGGCCT	TGGATGCCAG	GATTCCCCGC	AGTTGCC	GCCTGCCCA
1201	GCGNTACTGG	CAAATGCCGC	CCCTGTTTCT	GGAGCTGCTT	GGGAACCACG
1251	CGCAGTGCCC	CTACGGGGTG	TTCCTCAAGA	CGCACTGCC	GCTGCGAGCT
1301	GCGGTCAACC	CAGCAGCCGG	TGTCTGTGCC	CGGGAGAACG	CCCAGGGCTC
1351	TGTGGCGGCC	CCCGAGGAGG	AGGAACACAG	ACCCCGTGC	CCTGGTGCAG
1401	CTGCTCCGCC	AGCACAGCAG	CCCCCTGGCAG	GTGTACGGCT	TCGTGCGGGC
1451	CTGCCTGCGC	CGGCTGGTGC	CCCCAGGGCT	CTGGGGCTCC	AGGCACAACG
1501	AACCCGCTT	CCTCAGGAAC	ACCAAGAAAGT	TCATCTCCCT	GGGAAAGCAT
1551	GCCAAGCTCT	CGCTGCAGGA	GCTGACGTGG	AAGATGAGCG	TGCGGGACTG
1601	CGCTTGGCTG	CGCAGGAGCC	CAGGGGTTGG	CTGTGTTCCG	GCCGCAAGAGC
1651	ACCGTCTGCG	TGAGGAGATC	CTGGCCAAGT	TCCTGCACTG	GCTGATGAGT
1701	GTGTACGTGCG	TCGAGCTGCT	CAGGTCTTTC	TTTTATGTCA	CGGAGACCAC
1751	GTTCAAAAG	AACAGGCTCT	TTTCTACCG	GAAGAGTGTG	TGGAGCAAGT
1801	TGCAAAGCAT	TGGAATCAGA	CAGCACTTGA	AGAGGGTGCA	GCTGCGGGAG
1851	CTGTCGGAAG	CAGAGGTCAG	GCAGCATCGG	GAAGCCAGGC	CCGCCCTGCT
1901	GACGTCCAGA	CTCCGCTTCA	TCCCCAAGCC	TGACGGGCTG	CGGCCGATTG
1951	TGAACATGGA	CTACGTCGTG	GGAGCCAGAA	CGTTCCGCAG	AGAAAAGAGG
2001	GCCGAGCGTC	TCACCTCGAG	GGTGAAGGCA	CTGTTCAGCG	TGCTCAA
2051	CGAGCGGGCG	CGGCGCCCG	GGCTCCTGGG	CGCTCTGTG	CTGGGCGCTGG
2101	ACGATATCCA	CAGGGCCTGG	CGCACCTTCG	TGCTGCGTGT	CGGGGCCAG
2151	GACCCGCCGC	CTGAGCTGTA	CTTGTCAAG	GTGGATGTGA	CGGGCGCGTA
2201	CGACACCATC	CCCCAGGACA	GGCTCACCGGA	GGTCATCGCC	AGCATCATCA
2251	AACCCAGAA	CACGTACTGC	GTGCGTCGGT	ATGCCGTGGT	CCAGAACGGCC
2301	GCCCATGGGC	ACGTCCGCAA	GGCCTTCAAG	AGCCACGTCT	CTACCTTGAC
2351	AGACCTCCAG	CCGTACATGC	GACAGTTCGT	GGCTCACCTG	CAGGANAACA
2401	GCCCGCTGAG	GGATGCCGTC	GTCATCGAGC	AGAGCTCCTC	CCTGAATGAG
2451	GCCAGCAGTG	GCCTCTCGA	CGTCTTCCTA	CGCTTCATGT	GCCACACGC

FIG. 50A

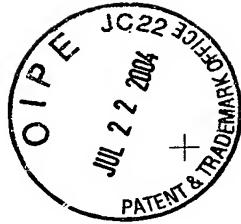
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2501	CGTGCATC	AGGGCAAGT	CCTACGTCCA	GTGCCAGGGG	ATCCCGCAGG
2551	GCTCCATCCT	CTCCACGCTG	CTCTGCAGCC	TGTGCTACGG	CGACATGGAG
2601	AACAAGCTGT	TTGCGGGGAT	TCGGCGGGAC	GGGCTGCTCC	TGCGTTGGT
2651	GGATGATTC	TTGTTGGTGA	CACCTCACCT	CACCCACGCG	AAAACCTTC
2701	TCAGGACCT	GGTCCGAGGT	GTCCCTGAGT	ATGGCTGCGT	GGTGAACTTG
2751	CGGAAGACAG	TGGTGAACCT	CCCTGTAGAA	GACGAGGCC	TGGGTGGCAC
2801	GGCTTTGTT	CAGATGCCGG	CCCACGGCCT	ATTCCCCTGG	TGCGGCCCTGC
2851	TGCTGGATAC	CCGGACCCCTG	GAGGTGCAGA	GCGACTACTC	CAGCTATGCC
2901	CGGACCTCCA	TCAGAGCCAG	TCTCACCTC	AACCGCGGCT	TCAAGGCTGG
2951	GAGGAACATG	CGTCGAAAC	TCTTGGGGT	CTTGCAGCTG	AAGTGTACAA
3001	GCCTGTTCT	GGATTGCA	GTGAACAGCC	TCCAGACGGT	GTGACCAAC
3051	ATCTACAAGA	TCCTCCTGCT	GCAGGCGTAC	AGGTTTACCG	CATGTGTGCT
3101	GCAGCTCCCA	TTTCATCAGC	AAGTTGGAA	GAACCCACAA	TTTTTCCCTGC
3151	GCGTCATCTC	TGACACGGCC	TCCCTCTGCT	ACTCCATCCT	GAAAGCCAAG
3201	AACCGAGGA	TGTCGCTGGG	GGCCAAGGGC	GCCGCCGGCC	CTCTGCCCTC
3251	CGAGGCCGTG	CAGTGGCTGT	GCCACCAAAGC	ATTCCCTGCTC	AAGCTGACTC
3301	GACACCGTGT	CACCTACGTG	CCACTCCTGG	GGTCACTCAG	GACAGCCCAG
3351	ACGAGCTGA	GTCGGAAGCT	CCCAGGGACG	ACGCTGACTG	CCCTGGAGGC
3401	CGCAGCCAAC	CCGGCACTGC	CCTCAGACTT	CAAGACCATC	CTGGACTGAT
3451	GGCCACCCGC	CCACAGCCAG	GCCGAGAGCA	GACACCAGCA	GCCCTGTCAC
3501	GCCGGGCTCT	ACGTCCCAGG	GAGGGAGGGG	CGGCCACAC	CCAGGCCCGC
3551	ACCGCTGGGA	GTCTGAGGCC	TGAGTGAGTG	TTTGGCCGAG	GCCTGCATGT
3601	CCGGCTGAAG	GCTGAGTGTC	CGGCTGAGGC	CTGAGCGAGT	GTCCAGCAA
3651	GGGCTGAGTG	TCCAGCACAC	CTGCCGTCTT	CACTTCCCCA	CAGGCTGGCG
3701	CTCGGCTCCA	CCCCAGGGCC	AGCTTTCT	CACCAAGGAGC	CCGGCTTCCA
3751	CTCCCCACAT	AGGAATAGTC	CATCCCCAGA	TTCGCCATTG	TTCACCCCTC
3801	GCCCTGCCCT	CCTTGCCCT	CCACCCAC	CATCCAGGTG	GAGACCCCTGA
3851	GAAGGACCT	GGGAGCTCTG	GGAATTGGA	GTGACCAAAG	GTGTGCCCTG
3901	TACACAGGCG	AGGACCTGC	ACCTGGATGG	GGGTCCCTGT	GGGTCAAATT
3951	GGGGGGAGGT	GCTGTGGGAG	AAAAATACTG	AATATATGAG	TTTTTCAGTT
4001	TTGAAAAAAA	AAAAAAA	AAAAAAA	AAAAAAA	+

FIG. 50B



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GCAGCGCTCGTCCTGCTCGCACGTGGAAAGCCCTGGCCCCGGCCACCCCGCGATGCC
 1 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
 CGTCGCACGCAGGACGACCGTGCACCCCTCGGGACCGGGCGGTGGGGCGCTACGG

a A A L R P A A H V G S P G P G H P R D A -
 b Q R C V L L R T W E A L A P A T P A M P -
 c S A A S C C A R G K P W P R P P P R C R -

GCAGCGCTCCCCGCTGCCAGCCGTGCCTCCCTGCTCGCACGCCACTACCGCGAGGTGCT
 61 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
 CGCGCGAGGGCGACGGCTCGGCACCGAGGGACCGACCGTGGTATGGCGCTCCACGA

a A R S P L P S R A L P A A Q P L P R G A -
 b R A P R C R A V R S L L R S H Y R E V L -
 c A L P A A E P C A P C C A A T T A R C C -

GCCGCTGGCCACGTTCGTGCAGCGCCTGGGGCCCCAGGGCTGGCGCTGGTGCAGCGCGG
 121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
 CGCGACCGGTGCAAGCACGCCCGGACCCGGGTCCCGACCGCCACAGTCGCGCC

a A A G H V R A A P G A P G L A A G A A R -
 b P L A T F V R R L G P Q G W R L V Q R G -
 c R W P R S C G A W G P R A G G W C S A G -

GGACCCGGGGCTTCGGCGCGNTGGTGGCCANTGCNTGGTGTGCGTGCCTGGGANGN
 181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
 CCTGGGCCGCGAAAGGCGCGNACCACCGGGTNACGNACCACACGCACGGGACCCCTNCN

a G P G G F P R ? G G P ? ? G V R A L G ? -
 b D P A A F R A ? V A ? C ? V C V P W ? ? -
 c T R R L S A R W W P ? A W C A C P G ? ? -

ANGGCNGCCCCCGCCGCCCTCCTCCGCCAGGTGTCCCTGCCTGAANGANCTGGTGGC
 241 -----+-----+-----+-----+-----+-----+-----+ 300
 TNCCGNCGGGGCGCGGGAGGAAGGCGGTACAGGACGGACTNCTNGACCACCG

a ? A A P R R P L L P P G V L P E ? ? G G -
 b ? ? P P A A P S F R Q V S C L ? ? L V A -
 c G ? P P P P P P S A R C P A * ? ? W W P -

CCGAGTGCTGCANANGCTGTGCGANCGCGCGCGAANAACGTGCTGGCCTTCGGCTTCG
 301 -----+-----+-----+-----+-----+-----+-----+ 360
 GGCTCACGACGTNTNCGACACGCTNGCGCCGCGCTTNTGACGACCGGAAGCCGAAGCG

a P S A A ? A V R ? R R E ? R A G L R L R -
 b R V L ? ? L C ? R G A ? N V L A F G F A -
 c E C C ? ? C A ? A A R ? T C W P S A S R -

GCTGCTGGACGGGGCCCGCGGGGGCCCCCGAGGGCTTCACCAACCAGCGTGCAGCTA
 361 -----+-----+-----+-----+-----+-----+-----+ 420
 CGACGACCTGCCCCGGCGCCCCCGGGGGCTCCGGAAGTGGTGGTCGACCGTGCAT

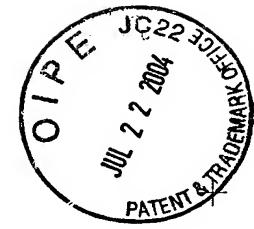
a A A G R G P R G P P R G L H H Q R A Q L -
 b L L D G A R G G P P E A F T T S V R S Y -
 c C W T G P A G A P P R P S P P A C A A T -

CCTGCCAACACGGTGACCGACGCACTGCCGGGAGCGGGCGTGGGGCTGCTGCG
 421 -----+-----+-----+-----+-----+-----+-----+ 480
 GGACGGGTTGTGCCACTGGCTGCGTGACGCCCTCGCCCCGACCCCGACGACGACG

a P A Q H G D R R T A G E R G V G A A A A -
 b L P N T V T D A L R G S G A W G L L L R -
 c C P T R * P T H C G G A G R G G C C C A -

FIG. 51A

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a P R G R R R A G S P A G T L R ? ? C A G -
 b R V G D D V L V H L L A R C A ? F V L V -
 c A W A T T C W F T C W H A A R ? L C W W -

 541 G G N T C C A G C T G C G C C T A C C A N G T G T G C G G G C C G C G C T G T A C C A G C T C G G C G C T G C N A C
 CCN A G G G T C G A C G C G G A T G G T N C A C A G C C C G G C G G C A C A T G G T C G A G C C G C G A C G N T G 600

 a G S Q L R L P ? V R A A A V P A R R C ? -
 b ? P S C A Y ? V C G P P L Y Q L G A A T -
 c ? P A A P T ? C A G R R C T S S A L ? L -

 601 T C A G G C C G G C C C C G C C A C A G C T A N T G G A C C C G A A N G C G T C T G G G A T C C A A C G G G C T
 A G T C C G G C C G G G G C G G T G T G C G A T N A C T G G G C T T N C G C A G A C C C T A G G T T G C C C G G A 660

 a S G P A P A T R ? W T R ? R L G S N G P -
 b Q A R P P P H A ? G P E ? V W D P T G L -
 c R P G P R H T L ? D P ? A S G I Q R A W -

 661 G G A A C C A T A G C G T C A G G G A G G C C G G G G T C C C C T G G G C T G C C A G C C C C G G G T G C G A G G G A G
 C C T T G G T A T C G C A G T C C C T C C G G C C C A G G G G A C C C G A C G G T C G G G C C A C G C T C C T C 720

 a G T I A S G R P G S P W A A S P G C E E -
 b E P * R Q G G R G P P G L P A P G A R R -
 c N H S V R E A G V P L G C Q P R V R G G -

 721 G C G C G G G G C A G T G C C A G G C G A A G T C T G C C G T T G C C C A A G A G G C C C A G G C G T G G C G C T G C
 C C G C G C C C C G T C A C G G T C G G C T T C A G A C G G C A A C G G G T T C T C C G G G T C C G C A C C G G G A C G 780

 a A R G Q C Q P K S A V A Q E A Q A W R C -
 b R G G S A S R S L P L P K R P R R G A A -
 c A G A V P A E V C R C P R G P G V A L P -

 781 C C C T G A G C C G G A G C G G A C G C C C G T T G G G C A G G G G T C C T G G G C C C A C C C G G G C A G G A C G C C
 G G G A C T C G G C C T C G C C T G C G G G C A A C C C G T C C C C A G G A C C C G G G T G G G C C C G T C C T G C G G 840

 a P * A G A D A R W A G V L G P P G Q D A -
 b P E P E R T P V G Q G S W A H P G R T P -
 c L S R S G R P L G R G P G P T R A G R L -

 841 T G G A C C G A G T G A C C G T G G T T T C T G T G T G T C A C C T G C C A G A C C C G C C A A G A A G C C A C
 A C C T G G G C T C A T G G C A C C A A G A C A C A C C A C A G T G G A C G G T C T G G G C G G C T T C T C G G T 900

 a W T E * P W F L C G V T C Q T R R R S H -
 b G P S D R G F C V V S P A R P A E E A T -
 c D R V T V V S V W C H L P D P P K K P P -

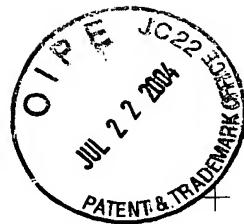
 901 C T C T T G G A G G G T G C G C T C T G G C A C G C G C C A C T C C C A C C C A T C C G T G G G C G C C A G C A
 G A G A A C C T C C C A C G C G A G A G A C C G T G C G C G G T G A G G G T G G G T A G G C A C C C G G C G G T C G T 960

 a L F G G C A L W H A P L P P I R G P P A -
 b S L E G A L S G T R H S H P S V G R Q H -
 c L W R V R S L A R A T P T H P W A A S T -

 961 C C A C G C G G G C C C C C A T C C A C A T C G C G G C C A C C A C G T C C T G G G A C A C G C C T T G T C C C C C G
 G G T G C G C C C G G G G G T A G G T G T A G C G C C G G T G G T G C A G G A C C C T G T G C G G A A C A G G G G C 1020

FIG. 51B

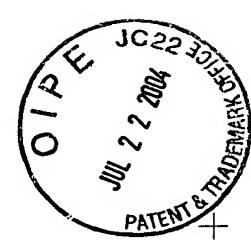
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FIG. 51C

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a S C G P A C A G W C P Q A S G A P G T T -
 b R A G L P A P A G A P R P L G L Q A Q R -
 c V R A C L R R L V P P G L W G S R H N E -

 AACGCCGCTTCCTCAGGAACACCAAGAAGATTCATCTCCCTGGGAAGCATGCCAAGCTCT
 1501 -----+-----+-----+-----+-----+ 1560
 TTGCGGCGAAGGAGTCCTTGTGGTCTTCAGTAGAGGGACCCCTTCGTACGGTTCGAGA

 a N A A S S G T P R S S S P W G S M P S S -
 b T P L P Q E H Q E V H L P G E A C Q A L -
 c R R F L R N T K K F I S L G K H A K L S -

 CGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCAGGACTGCGCTGGCTGCGCAGGAGCC
 1561 -----+-----+-----+-----+-----+ 1620
 GCGACGTCCCTCGACTGCACCTCTACTCGCACGCCCTGACGCCAACGACGCCGTCCCG

 a R C R S * R G R * A C G T A L G C A G A -
 b A A G A D V E D E R A G L R L A A Q E P -
 c L Q E L T W K M S V R D C A W L R R S P -

 CAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGT
 1621 -----+-----+-----+-----+-----+ 1680
 GTCCCCAACCGACACAAGGCCGGCGTCTCGTGGCAGACGCACTCCTCTAGGACCGTTCA

 a Q G L A V F R P Q S T V C V R R S W P S -
 b R G W L C S G R R A P S A * G D P G Q V -
 c G V G C V P A A E H R L R E E I L A K F -

 TCCTGCACTGGCTGATGAGTGTGTACGTCGAGCTGCTCAGGTCTTCTTTATGTCA
 1681 -----+-----+-----+-----+-----+ 1740
 AGGACGTGACCGACTACTCACACATGCAGCAGCTCGACGAGTCCAGAAAGAAAAACAGT

 a S C T G * * V C T S S S C S G L S F M S -
 b P A L A D E C V R R R A A Q V F L L C H -
 c L H W L M S V Y V V E L L R S F F Y V T -

 CGGAGACCACGTTCAAAAGAACAGGCTCTTCTACCGGAAGAGTGTCTGGAGCAAGT
 1741 -----+-----+-----+-----+-----+ 1800
 GCCTCTGGTGCAAAGTTCTGTCCGAGAAAAGATGGCCTCTCACAGACCTCGTTCA

 a R R P R F K R T G S F S T G R V S G A S -
 b G D H V S K E Q A L F L P E E C L E Q V -
 c E T T F Q K N R L F F Y R K S V W S K L -

 TGCAAAGCATGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCCAGCTGCGGAAG
 1801 -----+-----+-----+-----+-----+ 1860
 ACGTTTCGTAACCTTAGTCTGTGACTTCTCCCACGTCGACGCCCTCGACAGCCTTC

 a C K A L E S D S T * R G C S C G S C R K -
 b A K H W N Q T A L E E G A A A G A V G S -
 c Q S I G I R Q H L K R V Q L R E L S E A -

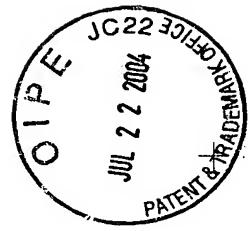
 CAGAGGTCAGGCAGCATGGGAAGCCAGGCCGCCCTGCTGACGTCAGACTCCGTTCA
 1861 -----+-----+-----+-----+-----+ 1920
 GTCTCCAGTCGCGTAGCCCTCGGTCCGGCGGGACGACTGCAGGCTGAGGCGAAGT

 a Q R S G S I G K P G P P C * R P D S A S -
 b R G Q A A S G S Q A R P A D V Q T P L H -
 c E V R Q H R E A R P A L L T S R L R F I -

 TCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTTGGAGGCCAGAA
 1921 -----+-----+-----+-----+-----+ 1980
 AGGGGTTCGGACTGCCGACGCCGCTAACACTTGTACCTGATGCAGCACCCCTCGGTCTT

FIG. 51D

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a S P S L T G C G R L * T W T T S W E P E -
 b P Q A * R A A A D C E H G L R R G S Q N -
 c P K P D G L R P I V N M D Y V V G A R T -

 CGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACGTGTCAGCG
 1981 -----+-----+-----+-----+-----+-----+ 2040
 GCAAGGGCGTCTCTTTCTCCCGGCTCGCAGAGTGGAGCTCCACTTCCGTGACAAGTCGC

 a R S A E K R G P S V S P R G * R H C S A -
 b V P Q R K E G R A S H L E G E G T V Q R -
 c F R R E K R A E R L T S R V K A L F S V -

 TGCTCAACTACAGAGCGGGCGCGCGCCCCGGCCTCCTGGCGCCTCTGTGCTGGGCTGG
 2041 -----+-----+-----+-----+-----+-----+ 2100
 ACGAGTTGATGCTCGCCCGCGCCGGGGCCGGAGGACCCGGAGACACGACCCGGACC

 a C S T T S G R G A P A S W A P L C W A W -
 b A Q L R A G A A P R P P G R L C A G P G -
 c L N Y E R A R R P G L L G A S V L G L D -

 ACAGATATCCACAGGGCTGGCGCACCTCGTGTGCGTGTGCGGGCCCAGGACCCGCCGC
 2101 -----+-----+-----+-----+-----+-----+ 2160
 TGCTATAGGTGTCCCGGACCGCGTGGAAAGCACGACGCACACGCCGGTCTGGCGCG

 a T I S T G P G A P S C C V C G P R T R R -
 b R Y P Q G L A H L R A A C A G P G P A A -
 c D I H R A W R T F V L R V R A Q D P P P -

 CTGAGCTGTACTTTGTCAAGGTGGATGTGACGGCGCGTACGACACCATCCCCAGGACA
 2161 -----+-----+-----+-----+-----+-----+ 2220
 GACTCGACATGAAACAGTTCCACCTACACTGCCCGCGCATGCTGTGGTAGGGGTCTGT

 a L S C T L S R W M * R A R T T P S P R T -
 b * A V L C Q G G C D G R V R H H P P G Q -
 c E L Y F V K V D V T G A Y D T I P Q D R -

 GGCTCACGGAGGTATGCCAGCATCATCAAACCCCAGAACACGTACTGCGTGCCTCGGT
 2221 -----+-----+-----+-----+-----+-----+ 2280
 CCAGAGTGCCTCCAGTAGCGGTCGTAGTAGTTGGGTCTTGTGCATGACGCACGCAGCCA

 a G S R R S S P A S S N P R T R T A C V G -
 b A H G G H R Q H H Q T P E H V L R A S V -
 c L T E V I A S I I K P Q N T Y C V R R Y -

 ATGCCGTGGTCCAGAAGGCCGCCATGGCACCGTCCGCAAGGCCTTCAAGAGGCCACGTCT
 2281 -----+-----+-----+-----+-----+-----+ 2340
 TACGGCACCAAGGTCTCCGGGGTACCGTGCAGGCGTTCCGGAAGTTCTCGGTGCAGA

 a M P W S R R P P M G T S A R P S R A T S -
 b C R G P E G R P W A R P Q G L Q E P R L -
 c A V V Q K A A H G H V R K A F K S H V S -

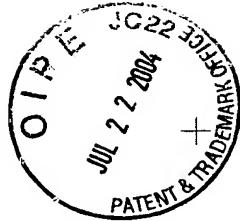
 CTACCTTGACAGACCTCCAGCCGTACATGCGACAGTCGTGGCTCACCTGCAGGANAACA
 2341 -----+-----+-----+-----+-----+-----+ 2400
 GATGGAACTGTCGGAGGTGGCATGTACGCTGTCAAGCACCGAGTGGACGTCCCTNTTGT

 a L P * Q T S S R T C D S S W L T C R ? T -
 b Y L D R P P A V H A T V R G S P A G ? Q -
 c T L T D L Q P Y M R Q F V A H L Q ? N S -

 GCCCGCTGAGGGATGCCGTGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTG
 2401 -----+-----+-----+-----+-----+-----+ 2460
 CGGGCGACTCCCTACGGCAGCAGTAGCTCGTCTCGAGGAGGGACTTACTCCGGTGTGTCAC

FIG. 51E

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a R * G M P S S S S R A P P * M R P A V -
 b P A E G C R R H R A E L L P E * G Q Q W -
 c P L R D A V V I E Q S S S L N E A S S G -

 2461 GCCTCTTCGACGTCTTCCTACGCTTACATGTGCCACACGCCGTGCGCATCAGGGGCAAGT 2520
 CGGAGAAGCTGAGAAGGATGCGAAGTACACGGTGGTGGCAACGCGTAGTCCCCGTCA

 a A S S T S S Y A S C A T T P C A S G A S -
 b P L R R L P T L H V P P R R A H Q G Q V -
 c L F D V F L R F M C H H A V R I R G K S -

 2521 CCTACGTCCAGTGCAGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCC 2580
 GGATGCAGGTACGGTCCCCTAGGGCGTCCCGAGGTAGGAGAGGTGCGACGAGACGTCGG

 a P T S S A R G S R R A P S S P R C S A A -
 b L R P V P G D P A G L H P L H A A A L Q P -
 c Y V Q C Q G I P Q G S I L S T L L C S L -

 2581 TGTGCTACGGGACATGGAGAACAGCTGTTGGGGATTGGCGGGACGGGCTGCTCC 2640
 ACACGATGCCGCTGTACCTCTGTTGACAAACGCCCTAACGGCCCTGCCGACGAGG

 a C A T A T W R T S C L R G F G G T G C S -
 b V L R R H G E Q A V C G D S A G R A A P -
 c C Y G D M E N K L F A G I R R D G L L L -

 2641 TCGCTTGGTGGATGATTCTTGTGGTACACCTCACCTCACCCACCGCGAAAACCTTCC 2700
 ACACGAAACCACTACTAAAGAACAAACCACTGTGGAGTGGAGTGGCTGGCTTGGAGG

 a C V W W M I S C W * H L T S P T R K P S -
 b A F G G * F L V G D T S P H P R E N L P -
 c R L V D D F L L V T P H L T H A K T F L -

 2701 TCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTAACCTGCGGAAGACAG 2760
 AGTCCTGGGACAGGCTCACAGGGACTCATACCGACGCACCACTGAACGCCCTGTGTC

 a S G P W S E V S L S M A A W * T C G R Q -
 b Q D P G P R C P * V W L R G E L A E D S -
 c R T L V R G V P E Y G C V V N L R K T V -

 2761 TGGTGAACCTCCCTGTAGAACAGCAGGGCCCTGGGTGGCACGGCTTTGTTAGATGCCGG 2820
 ACCACCTGAAGGGACATCTGCTCCGGGACCCACCGTGCAGAAAACAAGTCTACGGCC

 a W * T S L * K T R P W V A R L L F R C R -
 b G E L P C R R R G P G W H G F C S D A G -
 c V N F P V E D E A L G G T A F V Q M P A -

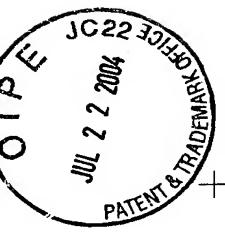
 2821 CCCACGGCCTATTCCCTGGTGCAGGCCCTGCTGGATACCCGGACCCCTGGAGGTGCAGA 2880
 GGGTGCAGATAAGGGACACGCCGACGACCTATGGCCTGGACCTCCACGTCT

 a P T A Y S P G A A C C C W I P G P W R C R -
 b P R P I P L V R P A A G Y P D P G G A E -
 c H G L F P W C G L L L D T R T L E V Q S -

 2881 GCGACTACTCCAGCTATGCCGGACCTCCATCAGAGCCAGTCTCACCTCAACCGCGCT 2940
 CGCTGATGAGGTGATAACGGGCTGGAGGTAGTCTCGGTCAAGAGTGGAAAGTTGGCGCCGA

FIG. 51F

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a A T T P A M P G P P S E P V S P S T A A -
 b R L L Q L C P D L H Q S Q S H L Q P R L -
 c D Y S S Y A R T S I R A S L T F N R G F -

 2941 TCAAGGCTGGGAGGAACATGCGTCGAAACTCTTGGGTCTTGCAGCTGAAGTGTACACA
 AGTTCCGACCCCTCTTGTACCGAGCGTTGAGAAACCCAGAACGCCGACTTCACAGTGT 3000

 a S R L G G T C V A N S L G S C G * S V T -
 b Q G W E E H A S Q T L W G L A A E V S Q -
 c K A G R N M R R K L F G V L R L K C H S -

 3001 GCCTGTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGA
 CGGACAAAGACCTAAACGTCACCTGTCGGAGGTCTGCCACACGTGGTTGTAGATGTTCT 3060

 a A C F W I C R * T A S R R C A P T S T R -
 b P V S G F A G E Q P P D G V H Q H L Q D -
 c L F L D L Q V N S L Q T V C T N I Y K I -

 3061 TCCTCCTGCTGCAGGCGTACAGGTTACCGCATGTGTGCAGCTCCCATTCATCAGC
 AGGAGGACGACGTCCGATGTCAAAGTGCACACAGACGTCGAGGGTAAAGTAGTCG 3120

 a S S C C R R T G F T H V C C S S H F I S -
 b P P A A G V Q V S R M C A A A P I S S A -
 c L L L Q A Y R F H A C V L Q L P F H Q Q -

 3121 AAGTTTGGAAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCCTCCCTGTCT
 TTCAAAACCTTCTGGGTGTAAAAGGACGCGCAGTAGAGACTGTGCCGGAGGGAGACGA 3180

 a K F G R T P H F S C A S S L T R P P S A -
 b S L E E P H I F P A R H L * H G L P L L -
 c V W K N P T F F L R V I S D T A S L C Y -

 3181 ACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGCCAAGGGCGCCGCC
 TGAGGTAGGACTTCGGTTCTGCGTCCCTACAGCGACCCCGGTTCCCGCGGCCGG 3240

 a T P S * K P R T Q G C R W G P R A P P A -
 b L H P E S Q E R R D V A G G Q G R R R P -
 c S I L K A K N A G M S L G A K G A A G P -

 3241 CTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCACTCTGCTCAAGCTGACTC
 GAGACGGGAGGCTCCGGCACGTACCGACACGGTGGTCTGAAGGACGAGTTGACTGAG 3300

 a L C P P R P C S G C A T K H S C S S * L -
 b S A L R G R A V A V P P S I P A Q A D S -
 c L P S E A V Q W L C H Q A F L L K L T R -

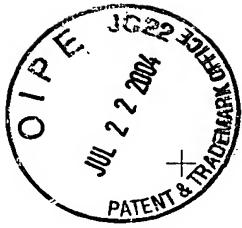
 3301 GACACCGTGTACCTACGTGCCACTCTGGGTCACTCAGGACAGCCCAGACGAGCTGA
 CTGTGGCACAGTGGATGCACGGTGAGGACCCAGTGAGTCCTGCGGTCTGCGTCAGT 3360

 a D T V S P T C H S W G H S G Q P R R S * -
 b T P C H L R A T P G V T Q D S P D A A E -
 c H R V T Y V P L L G S L R T A Q T Q L S -

 3361 GTCGGAAGCTCCGGGACGACGCTGACTGCCCTGGAGGCCAGCCAACCCGGCACTGC
 CAGCCTCGAGGGCCCTGTCGCACTGACGGGACCTCCGGCGTCGGTTGGGCCGTGACG 3420

FIG. 51G

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a V G S S R G R R * L P W R P Q P T R H C -
 b S E A P G D D A D C P G G R S Q P G T A -
 c R K L P G T T L T A L E A A A N P A L P -

 CCTCAGACTTCAGACCATCCTGGACTGATGCCACCGCCCACAGCCAGGCCAGAGCA
 3421 -----+-----+-----+-----+-----+-----+ 3480
 GGAGTCTGAAGTTCTGGTAGGACCTGACTACCGGTGGCGGGTGTGGTCCGGCTCTCGT

 a P Q T S R P S W T D G H P P T A R P R A -
 b L R L Q D H P G L M A T R P Q P G R E Q -
 c S D F K T I L D * W P P A H S Q A E S R -

 GACACCAGCAGCCCTGTCACGCCGGCTCTACGTCCCAGGGAGGGAGGGGCCACAC
 3481 -----+-----+-----+-----+-----+-----+ 3540
 CTGTGGTCGTGGGACAGTGCAGGCCCCGAGATGCAGGGTCCCTCCCTCCCCGCCGGTGTG

 a D T S S P V T P G S T S Q G G R G G P H -
 b T P A A L S R R A L R P R E G G G A A H T -
 c H Q Q P C H A G L Y V P G R E G R P T P -

 CCAGGGCCCGACCGCTGGGAGTCTGAGGCCCTGAGTGAGTGTGTTGGCCGAGGCCCTGCATGT
 3541 -----+-----+-----+-----+-----+-----+ 3600
 GGTCGGGGCGTGGCGACCCCTCAGACTCCGGACTCACTCACAAACGGCTCCGGACGTACA

 a P G P H R W E S E A * V S V W P R P A C -
 b Q A R T A G S L R P E * V F G R G L H V -
 c R P A P L G V * G L S E C L A E A C M S -

 CCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTG
 3601 -----+-----+-----+-----+-----+-----+ 3660
 GGCGCAGTTCCGACTCACAGGCCGACTCCGGACTCGTCACAGGTGGTCCCGACTCAC

 a P A E G * V S G * G L S E C P A K G * V -
 b R L K A E C P A E A * A S V Q P R A E C -
 c G * R L S V R L R P E R V S S Q G L S V -

 TCCAGCACACCTGCCGTCTCACTTCCCCACAGGCTGGCGCTGGCTCCACCCCCAGGGCC
 3661 -----+-----+-----+-----+-----+-----+ 3720
 AGGTGTTGGACGGCAGAAGTGAAGGGGTGTCCGACCGCGAGCCGAGGGTGGGTCCCGG

 a S S T P A V F T S P Q A G A R L H P R A -
 b P A H L P S S L P H R L A L G S T P G P -
 c Q H T C R L H F P T G W R S A P P Q G Q -

 AGCTTTCCCTCACAGGAGCCGGCTTCACTCCCCACATAGGAATAGTCATCCCCAGA
 3721 -----+-----+-----+-----+-----+-----+ 3780
 TCGAAAAGGAGTGGTCCCTGGGCCGAAGGTGAGGGGTGTACCTTATCAGGTAGGGTCT

 a S F S S P G A R L P L P T * E * S I P R -
 b A F P H Q E P G F H S P H R N S P S P D -
 c L F L T R S P A S T P H I G I V H P Q I -

 TTGCCATTGTTCACCCCTGCCCTGCCCTCCACCCACCATCCAGGTG
 3781 -----+-----+-----+-----+-----+-----+ 3840
 AAGCGGTAACAAGTGGGAGCGGGACGGGAGGAACGGAAGGTGGGGGTGGTAGGTCCAC

 a F A I V H P S P C P P L P S T P T I Q V -
 b S P L F T P R P A L L C L P P P P S R W -
 c R H C S P L A L P S F A F H P H H P G G -

 GAGACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTGGAGTGAACAAAGGTGTGCCCTG
 3841 -----+-----+-----+-----+-----+-----+ 3900
 CTCTGGGACTCTTCCCTGGGACCCCTCGAGACCCCTAACCTCACTGGTTCCACACGGGAC

FIG. 51H

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a E T L R R T L G A L G I W S D Q R C A L -
 b R P * E G P W E L W E F G V T K G V P C -
 c D P E K D P G S S G N L E * P K V C P V -

 TACACAGGCGAGGACCTGCACCTGGATGGGGTCCCTGGGTCAAATTGGGGGAGGT
 3901 -----+-----+-----+-----+-----+-----+ 3960
 ATGTGTCCGCTCCTGGACGTGGACCTACCCCCAGGGACACCCAGTTAACCCCCCTCCA

 a Y T G E D P A P G W G S L W V K L G G G -
 b T Q A R T L H L D G G P C G S N W G E V -
 c H R R G P C T W M G V P V G Q I G G R C -

 GCTGTGGGAGTAAAATACTGAATATATGAGTTTCAGTTTGAAAAAAA
 3961 -----+-----+-----+-----+-----+ 4020
 CGACACCCCTCATTTATGACTTATACTCAAAAGTCAAAACTTTTTTTTTT

 a A V G V K Y * I Y E F F S F E K K K K K -
 b L W E * N T E Y M S F S V L K K K K K K -
 c C G S K I L N I * V F Q F * K K K K K K -

 AAAAAAAA
 4021 ----- 4029
 TTTTTTTT

a K K K -
 b K K -
 c K K -

FIG. 51

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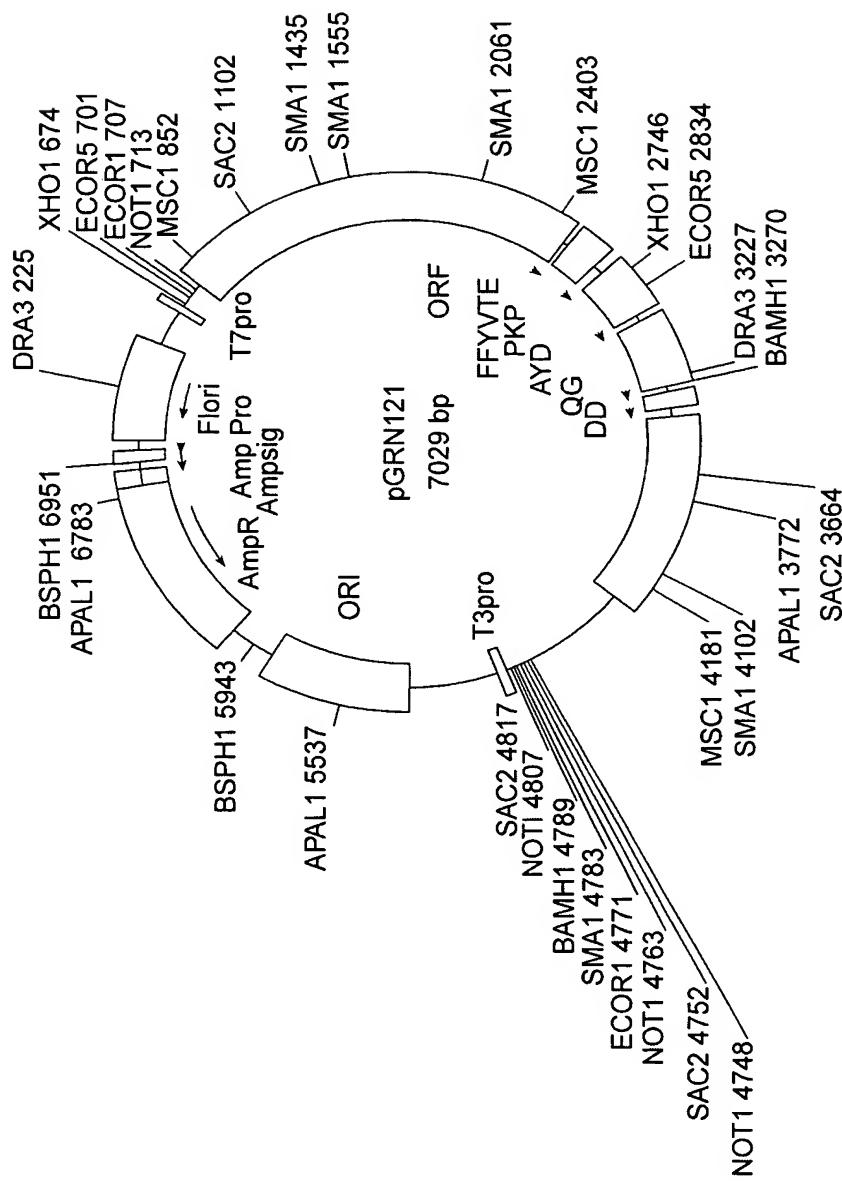
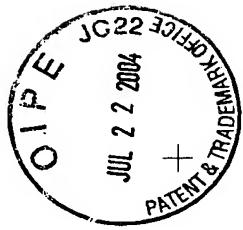


FIG. 52

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1
met

GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10

pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20

his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

30

gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

40

phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

50

ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

60

leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

70

gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TGC GCG CTG GAC GGG

80

ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

90

tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

100

trp gly leu leu leu arg arg val gly asp asp val leu val his
TGG GGG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

110

leu leu ala arg cys ala leu phe val leu val ala pro ser cys
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

120

ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

130

thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

140

150



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200 210
leu gly cys glu arg ala trp asn his ser val arg glu ala gly
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

220
val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

230 240
ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

250
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

260 270
ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

280
val val ser pro ala arg pro ala glu glu ala thr ser leu glu
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG
290 300
gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310
gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320 330
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350 360
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

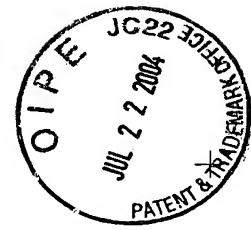
380 390
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410 420
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

FIG. 53B

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430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

440 450
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470 480
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500 510
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CAG GAG CTG ACG TGG AAG

520
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530 540
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560 570
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580
arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

590 600
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

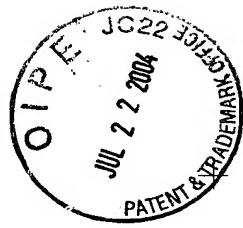
610
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620 630
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

FIG. 53C

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650 660
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CCC GGC CTC CTG

680 690
gly ala ser val leu gly leu asp asp ile his arg ala trp arg
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700
thr phe val leu arg val arg ala gln asp pro pro pro glu leu
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCT GAG CTG

710 720
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

740 750
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GGC

760
his gly his val arg lys ala phe lys ser his val ser thr leu
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

770 780
thr asp leu gln pro tyr met arg gln phe val ala his leu gln
ACA GAC CTC CAG CCG TAC ATG CGA CAG TTC GTG GCT CAC CTG CAG

790
glu thr ser pro leu arg asp ala val val ile glu gln ser ser
GAG ACC AGC CCG CTG AGG GAT GCC GTC GTC ATC GAG CAG AGC TCC

800 810
ser leu asn glu ala ser ser gly leu phe asp val phe leu arg
TCC CTG AAT GAG GCC AGC AGT GGC CTC TTC GAC GTC TTC CTA CGC

820
phe met cys his his ala val arg ile arg gly lys ser tyr val
TTC ATG TGC CAC CAC GCC GTG CGC ATC AGG GGC AAG TCC TAC GTC

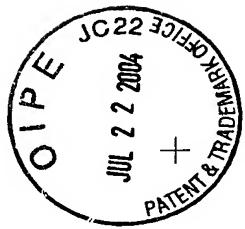
830 840
gln cys gln gly ile pro gln gly ser ile leu ser thr leu leu
CAG TGC CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC

850
cys ser leu cys tyr gly asp met glu asn lys leu phe ala gly
TGC AGC CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG

860 870
ile arg arg asp gly leu leu leu arg leu val asp asp phe leu
ATT CGG CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG

FIG. 53D

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880

leu val thr pro his leu thr his ala lys thr phe leu arg thr
 TTG GTG ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC

890

leu val arg gly val pro glu tyr gly cys val val asn leu arg
 CTG GTC CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG

910

lys thr val val asn phe pro val glu asp glu ala leu gly gly
 AAG ACA GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC

920

thr ala phe val gln met pro ala his gly leu phe pro trp cys
 ACG GCT TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC

940

gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
 GGC CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950

ser ser tyr ala arg thr ser ile arg ala ser leu thr phe asn
 TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC

960

arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
 CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

970

val leu arg leu lys cys his ser leu phe leu asp leu gln val
 GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

980

asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
 AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

1000

1020

leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
 CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1030

his gln gln val trp lys asn pro thr phe phe leu arg val ile
 CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1040

1050

ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
 TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1060

ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
 GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GGC CCT CTG CCC

1070

1080

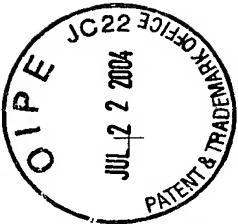
ser glu ala val gln trp leu cys his gln ala phe leu leu lys
 TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1090

leu thr arg his arg val thr tyr val pro leu leu gly ser leu
 CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

FIG. 53E

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1100 1110
 arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
 AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG
 1120
 leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
 CTG ACT GCC CTG GAG GCC GCA AAC CCG GCA CTG CCC TCA GAC
 1130 1132
 phe lys thr ile leu asp OP
 TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCACAGCCAGGCCAGAGCAGA
 CACCAAGCAGCCCTGTCACGCCGGCTCTACGTCCCAGGGAGGGAGGGGCCACACCC
 AGGCCCGCACCGCTGGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCAGGCCTGCATGTCC
 GGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTC
 CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTGGCTCCACCCAGGGCCAG
 CTTTTCYTCACCAGGAGCCCGGTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT
 CGCCATTGTTACCCYTCGCCCTGCCYTCCTTGCCTTCCACCCCCACCATCCAGGTGGA
 GACCCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTGGAGTGACCAAAGGTGTGCCCTGTA
 CACAGGGCGAGGACCCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC
 TGTGGGAGTAAATACTGAATATATGAGTTTCAGTTTGRAAAAAAAAAAAAAA
 AAAAAAA

FIG. 53F

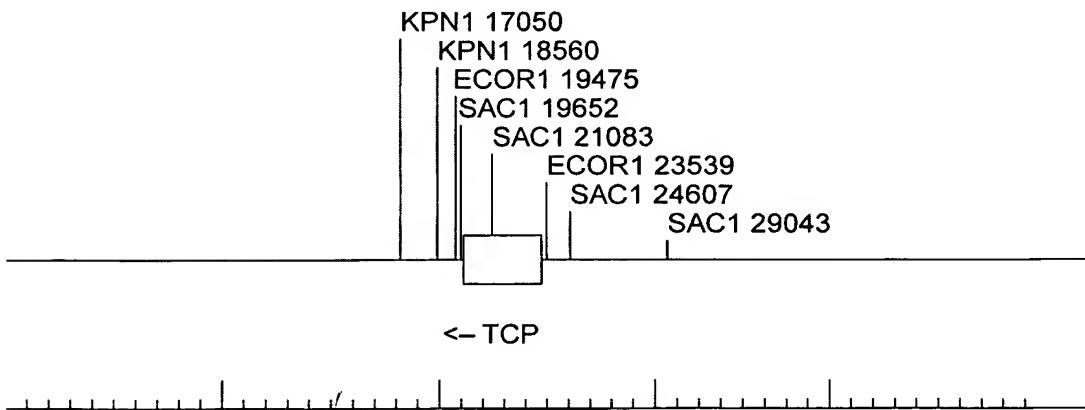


FIG. 54

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